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Minimum DB
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A_Geneseq_21:*
1: geneseqp1980s:*
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

RESULT 1 ADJ96642 ID ADJ9 antiinflammatory; enzyme; Nim-A related protein kinase; NRBP2. kinase; human; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease; metabolic; cardiovascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroprotective; immunomodulator; 06-MAY-2004 22-JAN-2004. WO2004006838-A2 Human Nim-A related protein kinase NRBP2 protein SeqID ADJ96642 standard; protein; 507 Homo sapiens. (first entry) A

99

15-JUL-2003; 2003WO-US021730.

L5-JUL-2002; 2002US-0395632P.

(SUGE-) SUGEN INC

Whyte D, Manning G, Caenepeel S;

WPI; 2004-122753/12. N-PSDB; ADJ96576.

New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., ca or neurological, immunological or inflammatory disorders. cancer,

Claim 1; SEQ ID NO 99; 366pp; English.

This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy

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Matches 507
                                   enzyme; protein kinase modulator; bioinformatics; diagnostic; cancer; central nervous system disease; psychotic disorder; neurological disorder; neurological disorder; neurodegenerative disease; metabolic disorder; cardiovascular disease; inflammatory disorder; gene therapy; cytostatic; antimigraine; analgesic; endocrine-gen.; nootropic; tranquilizer; hypotensive; hypertensive; neuroprotective; antiparkinsonian; virucide; fungicide; antibacterial; antidiabetic; anorectic; antiarteriosclerotic; ophthalmological; antiinflammatory; antiarthritic; antirheumatic; antiasthmatic; osteopathic; antipsoriatic; immunosuppressive; cardiovascular-gen.; vasotropic; antiallergic; gastrointestinal-gen.;
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7865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polypeptide sequence is a human kinase protein sequence of the invention.
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300

TAVDIFSFGMCALEMAVLEIQANGDTRVTEBAIARARHSLSDPNMREFILSCLARDPARR

IFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADG

PITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDT FITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDT

180 118 120

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179 181 119 121

59 61 Matches 476;

1 MAAPEPAPRRAREREREREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMD

MAAPEPAPRRG--REREREDESEDESDILEESPCGRWQKRREQVNQGNMPGIQSTFLAMD

88

TEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVI

TEEGVEVVWNELHFGDRKAFAAHEEKIQTMFEQLALVDHPNIVKLHKYWLDASEARARVI

Local

Similarity

.5e-234;

12;

Indels

8,

Gaps

Conservative

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cc acid molecules that encode kinase polypeptides. Specifically, it refers
cc to a bioinformatics strategy used to identify mammalian members of the
cc protein and lipid kinase families. The present invention provides methods
cc for identifying a substance that modulates the activity of a kinase
cc for identifying a substance that modulates the activity of a kinase
cc polypeptide, as well as a method for the detection of a kinase nucleic
cc acid in a sample as a diagnostic tool for a disease or disorder.
cc Furthermore, it describes generation of a knock-out mouse whose genome is
cc disrupted by recombination at a nucleic acid sequence such that it
cc produces a phenotype, relative to the wild-type, that exhibits an absence
cc of kinase activity. The nucleic acids and polypeptides given in the
cc specification are useful for the diagnosis and treatment of cancer,
cc entral or peripheral nervous system diseases, psychotic and neurological
cc disorders, neurodegenerative diseases, metabolic disorders, they can be
cc ardiovascular disease or inflammatory disorders. As such, they can be
cc ardiovascular disease or inflammatory disorders. As such, they can be
cc antimigraine, analgesic, endocrine-Gen., nootropic, tranquilizer,
cc hypotensive, hypertensive, neuroprotective, antiparkinsonian, virucide,
cc ophthalmological, antinflammatory, antiarthritic, antirheumatic,
cc ophthalmological, antipalematory, antiarthritic, antirheumatic,
cc ophthalmological, antiallergic and gastrointestinal-gen. This polypeptide
cc is a murine protein kinase of the invention.
                                    Query Match
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                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated, enriched, or purified kinase nucleic acids and polypeptides, useful for diagnosing or treating, e.g. cances neurological and neurodegenerative diseases, cardiovascular
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93.9%;
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Score 2499; DE
Pred. No. 5.5e-
11; Mismatches
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The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and disgnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to down regulate kinase capression and activity. Diseases related to kinase expression and activity. Diseases related to kinase expression and activity. Diseases related to my condition, of activity include rheumatoid arthritis, atherosclerosis, autoimmune constitutes, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative stress related disorders, chronic inflammatory bowel disease, chronic inflammatory political disease, autoimmunity disheres cancers and reproductives.
                                                                                                                                                                                                                                                                                                                                                                  neurodegenerative diseases and/or cancers
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   inflammatory pelvic
psoriasis, rhinitis,
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Best Local Similarity
Matches 460; Conser
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N-PSDB; ADI29379.
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Best Local S
Matches 460
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Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                        Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 181;
                                                                                                                                                                                                                                                                                                  460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RREQVNQGNMPGLQSTFLAMDTEEGVEVVMNELHFGDRKAFAAHEEKIQTVFEQLVLVDH
                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                   LTYDLLPTDSAQDLASELVHYGFLHEDDRMKLAAFLESTFLKYRGTQA
                                                                                                                                                                                                                                                                                                                                PRVLAPPPEEVQKAKTPTPEPFDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQ
                                                                                                                                                                                                                                                                                                                                                           PRVLAPPPEEVQKAKTPTPEPFDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                         EKTKAMDLHAVLAELPRPRRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSDPMMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSDPNMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALSFLHACSPPIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILS
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                                                                                                                                                                                                                                                              LTYDLLPTDSAQDLASELVHYGFLHEDDRMKLAAFLESTFLKYRGTQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EREELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNGDTRVTEEAIARARHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSN-----ALPDDLRSPIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILS
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                                                                                                          (first
                                                                        SEQ ID NO 1353.
                                                                                                                                                                           protein;
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98.3%;
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Pred.
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No. 2.9e-225;
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                                    gene therapy;
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Matches 355
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                        The invention relates to polynucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAMV8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111 (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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Ma Y,
                                                                                                                                                                                                                                                                                                                                   Sequence 357 AA;
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Y, Zhao QA,
AJ, Yang Y,
                                                                                                                                                                                                                                               145
                                                                                                                                                                                      205
                                                                                                                                                                                                                                                                          355;
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                                                                                                                                                                        PPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNG
                                                                                                                                                                                                                 MNARAWKRWCTQILSALSFLHACTPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSN---
IYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPPDSETRKVIQMQCNLERSEDKARW
                                                       CFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRPPLQWRYSEVSFMELDKFLEDVRNG
                                                                                                                  DTRVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAH
                                                                                                 DTRVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAH
                                                                                                                                                         ---ALPODIRSPIRAEREELRNIHFFPPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNG
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; 2000US-00560875.
; 2000US-00598075.
; 2000US-00620325.
; 2000US-0063325.
; 2000US-00633561.
; 2000US-00693325.
; 2000US-00728422.
                                                                                                                                                                                                                                                                          Conservative
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, Wejhrman
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ang D, Wang J
                                                                                                                                                                                                                                                                                      69.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g polypeptides with cytokine-like activities, useful therapy.
                                                                                                                                                                                                                                                                        Score 1858; DB 4;
Pred. No. 9.4e-172;
1; Mismatches 1;
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g J, Zhang J,
Goodrich R;
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J, Ren F,
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Best Local
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                       Sequence 326 AA;
                                                                                                                                                                                                                                                                        The present invention relates to human protein kinase. The proteins are from new human genes termed h12832, h14138, h1493, h15990, h15993, h16341 and h2252. The proteins may be used to identify modulators of their activity. The proteins may also be used to derive products for the treatment of cellular growth related disorders, malignancies, cancers, immune, inflammatory, respiratory, haematological and bone-related
                                                                                                                                                                                                                                                                                                                                                                                       New protein kinase polypeptides, nucleic acids and anti-kinase antibodies, useful for diagnosing and treating e.g. cancer, in immune, cardiovascular and bone disorders.
                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hodge MR,
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01-MAY-2000; 2000US-00562480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human h15993 protein
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IFIQHNGLIKIGSVWHRIFSNALRPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADG
                                                                                                                                                                                                                                                                                                                                                              Fig 13; 93pp; English.
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                                                             FITEYVSSGSLKOFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDT 180
                                                                                      TEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVI
                                                                                                          TEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSBACARVI
                                                                                                                                      MAAPEPAPRRAREREREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMD
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Pred. No. 1e-144;
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                                                                                 The present sequence is a novel protein kinase. The novel protein kinases CC and the nucleic acids that encode them may be used in the treatment and CC diagnosis of diseases associated with inappropriate kinase expression Such as immune-related diseases and disorders, cardiovascular disease, CC neurodegenerative diseases and disorders, cardiovascular disease, CC complementary sequences may also be used as DNA probes in diagnostic assays. The kinase expression and activity. Anti-kinase antibodies CC assays. The kinase expression and activity. Anti-kinase antibodies CC and kinase antagonists may also be used to down regulate kinase CC expression and activity. Diseases related to kinase expression and CC immune disorders, complications of organ transplantation, myocardial infarction, CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory bowel disease, chronic conflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, portiagis, rhinitis, autoimmunity, diabetee, cancers and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Fig 1; 310pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurodegenerative diseases and/or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding kinase polypeptides, useful for diagnosing treating immune-related diseases and disorders, cardiovascular dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dermatological; antidiabetic; antiinfertility; gene therapy; vaccin immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory pelvic disease;
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Query Match Best Local Similarity

57.5%; 61.6%;

Score 1534.5; Pred. No. 5.6

1.5; DB 4; 5.6e-140;

Length

535

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RESULT 8
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09-JUN-2000;
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11-JAN-2000;
                                                                                                            29-JUL-1999;
                                                                                                                          28-JUL-2000; 2000EP-00116126
                                                                                                                                           07-FEB-2001
                                                                                                                                                           EP1074617-A2
                                                                                                                                                                                          Human; primer;
                                                                                                                                                                                                           Human protein
                                                                                                                                                                                                                            26-JUN-2001
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                  2001-318749/34.
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                                Isogai T, Nishikawa
, Sugiyama T, Wakama
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                                                                        99JP-00248036.
99JP-00300253.
2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
for synthesizing polynucleotides, particularly the 5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                            (first
                                                                                                                                                                                                          sequence SEQ ID NO:12777
                                                                                                                                                                                         detection; diagnosis; antisense therapy; gene therapy
                                                          INST
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                                  Wakamatsu
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                                Hayashi K,
A, Nagai K,
                                Saito K,
C, Otsuki
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                                         Yamamoto
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length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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aim 8; SEQ ID NO 12777; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 full-CC length cDNAs defined in the specification. Where a primer set comprises:

((a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 complementary strand of a polynucleotide which comprises one of the 5602 coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a sequence and an oligonucleotide comprises a 3'-end sequence complementary to a coligonucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the coligonucleotide comprises a 1 least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers set can be used in antisense therapy and in comprise as a least 15 nucleotides and the combination of the specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the comprise and the comprise and the combination of the comprise and antisense therapy and in the comprise of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH3365 and AAH3653 to AAH3652 and coligonucleotides, all of which are used in the exemplification of the comprise and the comprises and the combination of the cDNAs easily without any specialised methods. AAH33629 to AAH36532 represent coligonucleotides, all of which are used in the exemplification of the comprises and the comprises and the combination of the combination of the comprises and

Sequence 535 AA;

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Query Match
Best Local Similarity
Matches 305; Conser
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                                                                                                                                                                                                                                                                                                                                                                                               RIFSNALRPTALFDDLRSPIRAERBELRNLHFFPPEYGEVAD-GTAVDIFSFGMCALEM
                                  RMKLAAFLESTFLKY 502
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                                                                         VVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEAD
                                                                                                          VIQMOCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFLHEDD
                                                                                                                                                 LDKFLEDVRNGIYPLTAF----
                                                                                                                                                                                                                       VPSLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLABIPAGPGREPVQTLYSQSPALE
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61.6%;
518
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Pred. No. 5.6e-140;
9; Mismatches 102;
                                                                                                                                                 GLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRK
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                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes assemblages and computer readable media comprising novel human cDNA sequences and clones derived from human foetal brain, foetal kidney, melanoma, testis and amygdala cDNA libraries. ABA93702 to ABA93766 represent human cDNA sequences from the present invention which encode the proteins given in ABB05662 to ABB05729. The human cDNA sequences and clones can be used in gene therapy. The clones may be used in a variety of applications, for example they may be used in profiling assays, for providing large arrays of human genetic material for implementing large-scale screening strategies and for treating diseases via gene therapy procedures
                                                                                                                                                                                                                                                                                                                                                           Sequence 535 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA sequences and kidney, melanoma, testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain derived protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB05696;
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                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                             VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFME
                                                                                                                                                                                                                     RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 216-217; 611pp;
                           AVLETQGNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFE
                                                                                                                                      KTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSV--
                                                                                                                                                                KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH 196
                                                                                                                                                                                          RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLK
                                                    AVLBIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE
                                                                                                         RIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVAD-GTAVDIFSFGMCALEM 255
                                                                                -----APDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEM
                                                                                                                                                                                                                                                                                                      Conservative
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61.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clones derived from human fetal brain, and amygdala cDNA libraries, useful in
                                                                                                                                                                                                                                                                                                     59;
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                                                                                                                                                                                                                                                                                                                   Score 1534.5; DB 5; Pred. No. 5.6e-140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                      Mismatches 102;
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                                                                                                                                                                                                                                                                                                                             Length 535;
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         The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, comprisite or allelic variation of the nucleic acid sequence. Also call sequence are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a compound to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the continuous first animal subjected to pain an animal subject of the continuous transfer to the continuous first animal subject of the composition.
                                                                                                                                                                                                                                                                                                   New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                     Example 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-268312/26.
GENBANK; NP_037524.
                                                                                                                                                                                                                                                                                                                                                                                                 Woolf C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2002; 2002WO-US025765
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29-JAN-2004
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(FARB ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in an animal of one or more of the polypeptides given in the
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(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                 two or more isolated polypeptides, treating pain in an animal.
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Matches 305
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                                                       cytostatic.;
                                                                              allergic disease; inflammation; autoimmune disease; diabetes; hyperlipidaemia; cancer; infection; HIV infection; antiallergic; human immunodeficiency; cancer; Thi hyperfunction; antiallergic; antiinflammatory; antidiabetic; antilipaemic; antiinfective; anti-HIV;
                                                                                                                                                                                          Human; STAT6-activating protein; drug screening; activator; inhibitor;
                                                                                                                                                                                                                                                 Human STAT6-activating protein,
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     Homo
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     sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                           entry)
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                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRK
                                                                                                                                                                                                                                                       ij
                                                    therapy; ribozyme therapy
                                                                                                                                                                                                                                                       NO:322.
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VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFME

329

VPSLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQTLYSQSPALE

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Matches 305;
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 acids. The invention also relates to recombinant vectors and host cells comprising a STAT6-activating protein-encoding nucleic acid; the recombinant production of a STAT6-activating protein; an antibody specific for a STAT6-activating protein; antisense oligonucleotides and ribozymes targeted to nucleic acids encoding a STAT6-activating protein; methods of screening for activators or inhibitors of STAT6-activating proteins; drug compositions comprising a modulator of STAT6-activating protein activity or expression; and methods of treating patients by administration of the drug compositions. The STAT6-activating proteins, nucleic acids encoding them, and modulators of their activity or expression are useful in the diagnosis and treatment of allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, cancer, infections (e.g., HIV), cancer and disorders associated with Thi hyperfunction. The present sequence is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001;
30-AUG-2001;
10-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAT6-activating proteins and encoded genes, applicable in diagnosis of and developing drugs to treat allergic diseases, inflammations, autoimmune diseases, diabetes, hyperlipidemia, infections e.g. HIV, and
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding them (ADG10411-ADG10894) and to sequences with you common their encoding bomology to the STAT6-activating proteins and their encoding homology to the STAT6-activating proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 322;
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                                  -----APDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEM
                                                      RIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPPEYGEVAD-GTAVDIFSFGMCALEM
                                                                                                                          KTKKNHKAMNARAWKRWCTQILSALSFLHACSFFIIHGNLTSDTIFIQHNGLIKIGSVWH
                                                                                                                                                                                              RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK
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 AVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE
                                                                                                                                                                         RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLK
                                                                                                                                                                                                                                               EEEEESEDESEILEESPCGRWQKRREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSE
                                                                                                        KTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSV--
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                                                                                                                                                                                                                                                                                                                57.5%;
nilarity 61.6%;
Conservative 59
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2001JP-00260681
2001JP-00313175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to 242 human STAT6-activating proteins (ADG10411-ADG10894) and to sequences with 95%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muramatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  즛
                                                                                                                                                                                                                                                                                                                ; Score 1534.5; DB 7; Pred. No. 5.6e-140; 59; Mismatches 102;
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RESULT 12
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Query Match
Best Local Similarity
Matches 305; Conserv
                                                                                                       The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3), that specifically hybridises with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative diseases, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                                                                                             New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                                                                 Sequence 535 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; antisense gene therapy; MARK3; MAP/microtubule affinity-regulating kinase 3; cancer; Alzheimer's disease; neurodegenerative disorde; hyperproliferative disorder; cytostatic.
                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 184; 233pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-2002; 2002US-00174319
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DB; ADI29382.
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   Conservative
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                57.5%; Score 1534.5; DB 8; 61.6%; Pred. No. 5.6e-140;
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   Mismatches
   102;
   Indels
                               Length
   29;
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EREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGD

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RESULT 13
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                                    WPI; 2004-459763/43.
N-PSDB; ADO58748.
                                                                Guegler
                                                                            Lal P,
                                                                                                                                                                                                 US2002058264-A1
                                                                                                                                                                                                                                                                               Human regulatory molecule HRM-20
                  New human
                                                                                                                            23-SEP-1997;
20-JAN-1999;
                                                                                                                                                         26-SEP-2001; 2001US-00840787
                                                                                                                                                                              16-MAY-2002
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                                                                 Hillman
KJ, Cor
                                                                                              INCYTE PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                VVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDKFLEDVRNGIYPLTAF----
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                                                                                                                 2000US-00518865
                                                                Corley
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99US-00234613.
                                                                            JL,
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                 useful in the
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes human regulatory molecules (HRM) (I) selected CC from a group comprising the fully defined amino acid sequences of SEQ ID CC NOs: 1-49. Also described are: an isolated polynucleotide (II) comprising CC a nucleic acid sequence encoding (I) or the complement of the polynucleotide (SEQ ID NOs:50-98); a composition comprising (II) and a creporter molecule; an expression vector containing (II); a host cell CC containing the vector; detecting (M1) expression of a nucleic acid in a csample; screening (M2) a plurality of molecules to identify a ligand; CC dagnosing (M3) a disease associated with gene expression in a sample CC containing nucleic acids; a composition comprising (I) and a plurality of molecules to identify a plurality of molecules an antibody which specifically binds to (I); and detecting protein expression in a sample. The new human regulatory protein compositions which are useful in the diagnosis and treatment of disease associated with cell proliferation, particularly immune cremitatory and cancers. This is the amino acid sequence of a human regulatory protein.
11-AUG-2005
                                  AEA61758;
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                                                                     AEA61758 standard;
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                                                                                                                                                                                                                              VIMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAABLVQLGFISEAD
                                                                                                                                                                                                                                                                                                                        LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEV-----QKAKTPTPEPFDSETRK 427
                                                                                                                                                                                                                                                                                                                                                                                                      VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFME
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                                                                   protein; 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%; Score 1534.5; DB 8; 61.6%; Pred. No. 5.6e-140;
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                                                                                                                                                                                                                    Best Local Similarity Matches 305; Conserv
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a candidate RAC pathway modulating receptor binding protein (NRBP) polypeptide or diagnosing or treating cancer.
                                                                                                                                                                                                                                                                                                         Sequence
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N-PSDB; AEA61756.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human nuclear receptor binding protein (NRBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFSEQ; NP_037524.
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                                                  RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLK
                                                                                       RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK 136
                                                                                                                                                                          EREDESEDESDILEESPCGRWOKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGD
        KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH 196
                                                                                                                                     EEEEESEDESEILEESPCGRWQKRREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSE
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                                                                                                                                                                                                                    59; Mismatches
                                                                                                                                                                                                                                          Score 1534.5; DB 9 Pred. No. 5.6e-140;
                                                                                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agent using a nuclear
nucleic acid, useful for
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KTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSV--

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RESULT:
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07-JUL-2000;
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26-JUL-2000;
14-AUG-2000;
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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04-FEB-2000;
24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001;
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       autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastroproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and prititalle bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and prititary dwarfism, cancers and disorders at the cellular level e.g.
                                                                                                                                                                                                                       Claim
                                                                                                                                                  novel central nervous system protein. (I) and polypept
by (I), are used to treat a medical conditions and in
pathological condition. Disorders which are diagnosed
                                                                                                                                                The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include
                                                                                                                                                                                                                                                                                                           N-PSDB; ABK43561.
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ring medical conditions and used as food
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Matches 305
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QSRLTSLLEETLNKF
                            RMKLAAFLESTFLKY
                                                                         LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEV-----QKAKTPTPEPFDSETRK
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                                                          VVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEAD
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                                                                                                                                                                                                          VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFME
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59; Mismatches
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preventing, additives or

disorders

involving neovascularisation e.g. malignancies,

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Result
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## ALIGNMENTS

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	rce E S S M	AR448352 LOCUS DEFINITION Sec ACCESSION AR4 VERSION AR4 VERSION AR4 VERSION AR4
y: rity:	Unknown. Unclassified. Unclassified. Unclassified. 1 (bases 1 to 4048) 1 (bases 1 to 4048) Furness, L.M. and Buc Genes expressed in C Genes: US 6673549-A Incyte Corporation, Location/Qu 1. 4048 /organisms-m/ouglass-m	AR448352 Sequence 105 AR448352 AR448352.1
1.16e-213 2612.00 98.62% 98.62% 97.83%	Unknown.  Unknown.  Unclassified.  1 (bases 1 to 4048)  1 (bases 1 to 4048)  Furness,L.M. and Buchbinder,J.L.  Genes expressed in C3A liver cell cultures treated with steroids patent: US 6673549-A 1053 06-JAN-2004;  Incyte Corporation; Palo Alto, CA  Location/Qualifiers  1. 4048  /organism="unknown" /mol_type="genomic DNA"	AR448352 Sequence 1053 from patent US 6673549. AR448352 AR448352.1 GI:42676676
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                                                                               Strausberg, R. D., Collins, F.S., Wagner, L., Schumen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Bhat, N.K., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malak, J.A., Gunaratne, P.H., Rtchards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Vallalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Pahey, J., Hetton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Homo sapiens hypothetical protein LOC340371, mRNA (cDNA
IMAGE:4375917), partial cds.
   Strausberg, R.
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1 (bases 1 to 3892)
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Mammalia; Eutheria;
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33 09 53	93 AlaThrArgProLeuGlyLeuProArgValLeuAlaProProProGluGluValGlnLys	73 GluLeuAspLysPheLeuGluAspValArgAsnGlyIleTyrProLeuMetAsnPheAla 	53 GluLeuProArgProArgProProLeuGlnTrpArgTyrSerGluValSerPheMet 372 	33	25 Cy8PhelleGlnHisGlnTyrLeu 332 	05 SerLeuLeuPheHisArgValLeuPheGluValHisSerLeuLysLeuLeuAlaAlaHis 324 	85 MetArgGluPheIleLeuCysCysLeuAlaArgAspProAlaArgArgProSerAlaHis 304 	65 AspThrArgValThrGluGluAlaIleAlaArgAlaArgHisSerLeuSerAspProAsn 284 	45 IlePheSerPheGlyMetCysAlaLeuGluMetAlaValLeuGluIleGlnThrAsnGly 264	25 ArgasnLeuHisPhePheProProGluTyrGlyGluValAlaAspGlyThrAlaValAsp 244 	05 ProProThrAlaLeuProAspAspLeuArgSerProIleArgAlaGluArgGluGluLeu 224	92 GlySer	72 IleHigGlyAspLeuThrSerAspThrIlePheIleGlHHigAspGlyLeuIleLygIle 191 	ArgTroCysThrGln11eLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIne	Ly8GlnPheLeuLy8Ly9ThrLy8Ly8AsnHisLy8AlaMetAsnAlaArgAlaTrpLy8 	12 ThrSerGluAlaCysAlaArgValllePheIleThrGluTyrValSerSerGlySerLeu 131 

Oy 140 LysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGlnIleLeuSer 159	Qy 100 ProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCysAlaArgVal 119	Qy 60 AspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAspArgLysAla 79	Indels: 6 Gaps: 7) x AX056416 (1-3304) 70 y AX056416 (1-3304) 10 y AshmetProGlyLeuG	/db_xref="taxon:9606"  ment Scores: .No.: 2.3e-196 Leng .209.00 Matc .Not Similarity: 98.72% Const .Cocal Similarity: 98.29% Mism	AUTHORS Plowman, G.D., Martinez, R., Whyte, D. and Sudersanam, S. TITLE Protein kinases JOURNAL Patent: WO 0073469-A 60 07-DEC-2000; Sugen, Inc. (US) FEATURES Location/Qualifiers source /organism="Homo sapiens" /mol type="unassigned DNA"	-	Db 1369 GAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTCCCAACGACAGCGCCCAGGAC 1428  Qy 473 LeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAspArg 488
Qy 500 LeuLysTyrArgGlyThrclnAla 507		Oy 420 ProbheAspSerGluThrArgLyValIledInMetGlinCysAsnLeuGluArgSerGlu 439	AspValArgAsnGlyIleTyrProLeuMetAsnPheAlaAlaThrArgProLeuGlyLeu		Qy 300 ArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGluValHisSerLeuLys 319	Qy 260 IleGlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArgHisSer 279	Qy 180 ThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArgIlePhe 199

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40 ArgArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPheLeuAlaMet 59 :::     :::	es: rity: ilarity:	8 L	/gene="DKFZp434P086" 7991575 /gene="DKFZp434P086" /note="similarity to C.elegans H37N21.1/K10D3.5" /codon_start=1 /product "hypothetical protein" /protein_id="CAB70864.1" /db_xref="GOA:Q9NSYO"	W	sequence Berlin/G Genome P This Clor Please co Berlin-Cl informati	AL137662 AL137662.1 GI:6807782 Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Mammaila; Eutheria; Euarchonto Hominidae; Homo. 1 (bases 1 to 3538) Koehrer,K., Beyer,A., Mewes,H. Direct Submission Submitted (15-JAN-2000) MIPS, Martinsried, GERMANY Clone from S. Wiemann, Molecul
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Rarren, B., Linton, L., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Chang, J., Chazaro, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Goode, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gonde, S., Gord, S., Govette, M., Graham, L., Grand-Pierre, N., Hagoo, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karlas, A., Kells, C., LaRocque, K., Jones, R., Karatas, A., Kells, C., LaRocque, K., Jones, R., Karatas, A., Kells, C., LaRocque, K., McCarthy, M., WcEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Mencarthy, M., WcEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Norbb, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Traylis, N., Traylilo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., M., Traylis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., M., Traylis, N., Traylino, J., Ye, W.J., Young, G., Enhett M., Zimmer, A. and Zody, M.
                                                                        REBEGLEH, 340 CHBLIES STREET, CAMBRINGE, MA U2141, USA

Allen, N. Bases I to 92291)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

Boyuslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,

Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,

Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,

Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,

Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy T., Naylor, J.,

Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,

O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,

Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,

Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,

Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
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Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (22-DEC-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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FEATURES
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or accession nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 2, 2003 this sequence version replaced gi:28827929.

All respeats were identified using RepeatMasker:
smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Only the middle 92.3 kilobases of this clone are being submitted. The remainder overlaps either accession number AC109322 [WICGR
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Location/Qualifiers
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complement (4473. .4777)
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/rpt_family="LIMD2"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="RP11-299M14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'chromosome="8"
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ement(6340)
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complement(15346. .15495)
/rpt_family="MLTIC"
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8208. .85
                                                                                                                                                                                                                                                                                                                         complement (18519. .18684)
/rpt_family="L2"
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17753. .17057
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/rpt_family="Aluy"
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complement(14215. ...
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7326. .7349
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0697. .10994
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ement(16477
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ement(1221)
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                                                                                                                                                                                                                                                                                                                                                                                                            family="MER30"
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	Qy       122 leThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLysLysAsnH 142         Db       1
7 gValThrGluGluAlaIleAlaArgAlaArgHisSerLeuSerAspBroAsnMetArg	20448 CATGGGGACGAACCCGCAGCTGGTGGAAATCCTGAGCTCGCACCGTGCAGGTCATCTTCA 20507
255	Qy 119
6 GCTCTGCCCTCCTAACTGTGCCCTGCCTGGCTCACCTGTGTGTG	QY 116 BALBARG 118
	Db 20328 GGTGGACCACCGGAACATCGTGAAGTTGCACAAGTACTGGCTGG
<b>1</b> ω	96 uValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCy 116
7 GCTTCTCTCCTACGTGTCCTGTGCTCTCTTCTGTTCAGAGGTGGCCGATGGGACCGCTGT	QY 85GluLysIleGlnThrValPheGluGlnLeuValLe 96
7	QY 82 AlaHiBGlu
21227 TCCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACTTCGGAACCTGCACTT 21286 229 ePheProProGluTyrGly 235	201
9 uProAspAspLeuArgSerProIleArgAlaGluArgGluGluLeuArgAsnLeuHisPh	62 GluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAspArgLysAlaPheAla 81
7 GGGGGGACGGGGTCCTGGAGAGGTCCCCGCCCGCTCAGCTCTGCGCCCTCCCACAGCACT	Qy         45AsnGlnGlyAsnMetProGlyLeuGlnSerThrPheLeuAlaMetAspThr 61
3LeuArgProProThrAlaLe	Db 20028 GGACCAAATCCTCACCCACAACCCTGACACACACACACAC
931162	Oy 44 44 Th
B GGGAAGGTGCCTGGAGCCAAGGGGAAGTTCTGATGCCCCAGCAGCTAACTCCACTC	19968 CCCGCAGAGTGGCTCAGGGCCTGCAGCCCCACGCTTGGGCCCACTGGAAAGGTGTGGACAG 20027
3	44
B GGCCTCATCAAGATCGGCTCCCGGTGCTGGCGGGGCAGGGCTGGGTGGG	19908 CCCAGCCCTTGGATAGGAGCCCTTGGCTCCTGGGGGGGAGCTACCCTCCAAGCCCCACCTT 19967
7 GlyLeuIleLysIleGlySer	44 44
8 TGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGACACCATCTTCATTCA	198
7 CysSerProProIleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHisAsn	44 44
20868 AGCCTCCTGACCGGCTCCTCCTACTCTCCCCCAACGTCTGCAGCTTCCTGCACGCC 20927	Db 19788 CCCTGGGACTCCCTGAGGGCCAGTCTCCCTCCCCAGGACCACCTCCCCATGCCTCTGGAACTC 19847
161Leu-SerPheLeuHisAla 166	19728 TCCGCGGCCCCTCGCGGGCCCGCGAATCAGCCACCCCTGGACCCCTTTGGCCTGGCGCTCG 19787
20808 CGCTCAGGTGAGGCCTGGGCTGGGCCTGGGCGCGCCGAGCCCGAGCCCCATCTCTCCAG 20867	Qy 44
8	19668 GGGGCCTGGAGGCTGCGCGGGGCGTGGGGGCGCTGGGAGAGCGCGGCGGCGGAAAACCTC 19727
о 6	44
CTGGGCGAGGATGCGGGGCGGGCTCCGCAGGCCCAGCCTCTCCTGCGCCCACCCGAC	
148 148	41 Aroginginvaj
8 GGTTGGGGCCAGCCTCGGGGACTGGGAATGGTGAGGGGGTGCCCCGGCGGCCTCGGACAGGGG	Qy 21 GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg 40  Db 19549 GACAGCGACGACCGACGTCGGACGACAGCACGACGCACGC
148	19548
	Oy 1 MetAlaAlaProGluProAlaProArgAlaArgGluArgGluArgGluArgGluAsg 20

Db 22726 TGGCTGGGGAGGTTGGGACGTGGAAGGGGCCCTGCAGGACCCACGGCCTGAGCA 22785	Qy 329 329	Db 22666 GCTCCTGGCAGCCCACTGCTTCATCCAGCAGCAGCAGCAGCAGGCCGGGGGGG 22725	329	22606 CCGGCCCTCTGCCCACAGCCTCCTCTTCCACCGCGTGCTCTTCGAGGTGCACTCGCTGAA 22665	319		299	Db 22486 CTCAGGGGCCACCTCTCCTCGAACTGCGGGCCAGAGCAGAGAGCCCTTGCACACCACCA 22545	Qy 286 286	Db 22426 GACTCCTCCCTATGGGCATCCCTGCATGTCCTGTGTGTCCCTGAGGAGGGACATGGGGAA 22485	286	Db 22366 CCAGAACCCAGCTGTCCTCAAGCTCAGAGGACCAGGTCCTGGCCTGGCTGCTGCTGCTGG 22425	Qy 286 286	Db 22306 TCATGGCTTCTCCCCACGATTTTTTGGGGGTCGAGGGAAGCAGAGCATGGTGCTCCAATC 22365	Qy 286 286	Db 22246 GGCCCGAGCTGAGCCGATCAAAAGGCCATGGGTAGGAGGCTTGCAGGTGTGACTTTAGGA 22305	Qy 286 286	Db 22186 AGCCGGGCTGGGCACGGATGTGGACAGAGTGGGGACCCCATCAAGGTCGTCTCCAGTGTTG 22245	Qy 286 286	Db 22126 AGACTTAACTCCATGGCCTCAGGAGATGGGGGTGCCTGGTCGGGGGTGGCGAGCTGG 22185	286 286	Db 22066 AGCAGGCAAAAAAGGTATGGGATGGAAGCTGCATCCACAGCCCCCTCTGCTCGGAGTCT 22125	Оу 286 286	Db 22006 GACTTTAAGCTTCCAGGAGGTGATGAGGCTCCAGCTTGTGGGGGGGACATGGTGGGTG	Oy 286 286	Db 21946 GCTTTAGAGTGAGTGGAGCCAACATCTGCACCTGGGTCTGCTTCACTCCAAGTCCTT 22005	Оу 286 286	Db 21886 ATCACCATGCCCGTTTTATAAAGAAACCAAGGTTCAGAGGAGATGAGTCCTTTGCCCAAG 21945	Оу 286 286	Db 21826 TAAGGGGTCAGCACATTCTAAGGACAAGAAGGCAAGAGACACCTCCCTC	Оу 286 286	Db 21766 TGCACCCCTCCCAAAGAGGACCTCAGTGGGAGCACATACTGGTTCCAGGCCTGAAGGCCC 21825	Оу 286 286	Db 21706 GCTCCAGGCAGACCTGGGAGAACATCACAGTTTGTGCAGTTGAGGGGGTATACCAGCTGAC 21765	
Db 23802 GTCCTCAGCTGACGCCCAGGCTCTGGGAGGCCTGATCCCGCAGGCACCGTGCACTTCGGC 23861	428	23742 CAGAATTCATGTCCTAACAGGCAAACTGCCTGCTCCTGGCTGCCAGCAGAGATCATGGGA	Qy 428 428	23	Qy 428 428	Db 23622 CCCCCACCCTCCCATCCCCACCTGGTGCTGATTCCCGGACATCTATGTCCTGGTGTCT 23681	Qy 428 428	Db 23562 CACCCGGGCTCTTCCACCCTGCCAGCAATCTTCCCCCACCCCGCACCCCTCCCACCCCC 23621		23	Qy 428 428	Db 23442 GGGGTTATAGGACAGGCTGGGCACTCTCCTTTTCCGGGAGGCTCCCTTGTCCCCTCAGAT 23501	Qy 428 428	23	428	23	4.00	478 478 - ATTI MAKTIKTANAN KATI-BANGTIKKKI TIKTIBKTAKTIKATISKKATIKKKI TA		420 Obbohondord in Thranci wolfer	1	23143 CCCAGGAATGAAACCTACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTGCC		23083 TGATGTAAGSTTGGGGCCAGGCAGCCTGTCAGGCCTGAACCCCCAGCCACCCTGTTGTGT		z3 V24 GIRCICGGRAGICICCTICATGGRGCTGGRCAARTFCCTGGRGGRTGT-CRGGTGRGARAC	366 - TyrsersiuvalserPheMetGluLeuAapLyaPheLeuGluAapVal	23964 CCGCACCTCCCCTCCCCCCCCGGCCAGCCCCTCATGTGCCTCCCACTTCCATGCCAG		226 269 GETARMATARA ATARA MATEMATEMATEMATEMATEMATEMATEMATEMATEMATE		22845 GACCAAGGCCATGGACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGCAGGCCCCC	31 SILLLYBALAMERASDIEURISAIAWAILDEALAGIUEUFFOARGFFOARGARGFROFF	22/86 CACCGCCTTGATGCCTTGTGGCCGCAGAC-CTCATGCCTGAGAATGTGGTGGAGGAGAAA	

		Euarchontoglires; Glea; Muridae; Murinae (9) and Lander,E. come 15, clone RP23-4
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All repeats were i Smit, A.F.A. & Gre http://ftp.genome.		Db 24641 AGTACCGTGGGACCCAGGCC 24660
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Vo,A., Wilson,B., Zimmer,A. and Zody		24
		Qy 485 485
O'Connor, T., O'Don Phunkhang, P., Pier Retta, R., Rise, C.,		Qy 471 lnAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGlu
<pre>MacLean, C., Macdon McCarthy, M., Meldr Murphy, T., Naylor,</pre>		Db 24402 CGGCGGGTGGGCAGCGGCCTCATGCCTCGCCTTACGCCATTGCCTCAGCGGACAGCGCCC 24461
		Oy 467Thr-AspSerAlaG 471
H G F		Qy         461 rTyrhspleuleuPro
Bloom,T., Boguslav Choepel,Y., Collym		24282 GCCGCCTCCCCAGCTCTCTGCTTCTGGTGCTGGAAGACCGGCTGCACCGGCAGCTGAC
	AUTHORS	Oy 446LeuThrLeuLeuLeuLeuCulaACCCTGAACCCGCGAGCGAGCCAGGCCC 24281
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	TITLE	24162 CAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCATGTGAGCGGGGCCTGGGAGGGCGG
N., Subi		Oy 433 sAsnLeuGluArgSerGluAspLysAlaArgTrpHis 445
Raymond, C., Retta, Roman, J., Rosetti, Seaman, S., Severy,		Db 24102 TCTTGCTGGGGTTTGTGAGTCCCAGCCTTCCCCCGGTGCAGGTCATCCAGATGCAGTG 24161
Norbu, C., Norman, C Oliver, J., Peterso		Db 24042 ATTCCCCCCTTTCCAGTCTTTGCTGTCCCTTCCCGGCCCCTTTGGGGCCGCGGCATGTGG 24101
McCarthy, M., McEwa		Qy 428
·		Db 23982 CTTCTCGAAGCTTTCCTTAGCTTGCCAAGCCACTAGCAGTGAGATGGGCTCCTCTTAGAG 24041
• •		Qy 428 428
ъC		Db 23922 TGTTCTCTCCGCGGTGAAAGCTCCTATTCAGCCTTCAGTACCCAGCCCCTAATGTCGACT 23981
<b>B</b> C		Qy 428 428
	AUTHORS	Db 23862 GCGGTCCTGTCCCGCCCAACCTCCCTTTCCCCACGCCCACAGTTCCCTCTTTGTTCAAGT 23921
	REFERENCE	Qy 428 428

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a 'working draft' sequence. It currently contigs. Gaps between the contigs days between the contigs days for the pieces be correct as given, however the sizes tween them are based on estimates that have

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85	74 PheGlyAspArgLysAlaPheAlaAlaHisGlu	54 SerThrPheLeuAlaMetAbpThrGluGluGlyValGluValValTrpAsnGluLeuHis 73	45	5959 AGCACATTCACGGCTGGGGGAAGGTTGTGGCGGAGACCACGTCCACACCCTGGGTCTATT 6018	5899 TGGGTTCTTGATTCCCAGCCTTACCTCCTCAGCCCTCCCACTGAGCTGGGCAAGGCTAGC 5958	5839 CCCAACCTCTAAAACCTGCGTACCTTCTGGCCCAGCCCTGGACACCACCCTTCTCCCCC 5898		44 44 5779 TGTCATACTGGGACCACCTCCACGTGCCTCTTGGATCCCTACTACCGCTCTGGGGATCTC 5838	5719 GGCCCTCGGATCCCTTTGGCCCCAAGCCCTGGTGAGAAACCCCCCATTCCTTGAACACCGG 5778		5659 CCATGGGATCCGTGGGGCCGAGCCAGTATGAGGGTCTCCCCCGGACGCCCTGGCCTCTGGA 5718	coording to the control of the contr	4. 7	21 GIUSETGIUASPGIUSETASPITELEUGIUGIUSETPTOCYSGIYATGTTPGINLYSATG 40 		618-941-99 (1-507) x AC116487 (1-174949)	58.56% Indels: 14 Gaps:		ent Scores:		/db_xref====================================	rce *
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727 AGAACTGACCAACGCTGTCTTGCTTCTCCCATTTCAGAAGTCAATGATGGGACTGCTGTG 7336	31 roproglutyG1y	1 SpaspheuargserFrolleArgalaGluArgGluGluLeuargAsnLeuhlsPhePhePhePhePhePhePhePhePhePhePhePhePheP	97 GTGTGGGGACCATGGAGAAACTTGTCTTTAGCTCCACCCTTTTCCTCAGCACTTCCTG	TGCGTTGGCTGTTGCAGTGTGGTAGTGTGTGGGGTCTCTGGGG	6977 GGGAGCCCTGGACAGAGACTGCCCAGTCTCCCCGCCCAACTGACATCCTGTCTTTTCTCTC 7036	193 193	90 slleGlySer	170 OllelleH18GYYASDLeuThrSerAspThrILePheILeGInH18ASDGLYLeuIleLy 190	97 CCGGTTCTTCCTGCCTCTCATCCTCTATGCTTGCAGTTTTTTGCACGCCTGCAGTCCCCC	162 SerPheLeuHisAlaCysSerProPr 170	6737 AGAGCCTGGCCTTGCCCACGCGCTTGCCCCCTGCTCTGCACCTTTCCGCTGCTCTCTGAC 6796	161 161	149AlaTrpLysArgTrpCysThrGlnIleLeuSerAlaLeu 161	GTGGGGTAGCGGGCGGCTCCGCAGGCTCAGCAGCCTTTTGGTGCCCACCCGACGGAGTC	6557 GTCCAGCAGAACTTAGGGACAGTAGTGGGGGGGGGGGGACTCCGGAAAAAACCTCGGTTCAGGA 6616	148	39 LysLysAsnHisLysAlaMetAsnAlaArg 148	119 ValilePheIleThrGluTyrValSerSerGlySerLeuLy8GlnPheLeuLy8Ly8Thr 138 		116Cysalaarg 118	11 AspThrSerGluAla	91 PheGluGlnLeuValleuValAspHisProAsnIleValLysLeuHisLysTyrTrpLeu 110 

Qy 334 roGluAsnValQuGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluL 354	Db 8116 TGAGGGGCAGAAGGGCCGGGGTGGGTCAGGATCCTGGGGTCAGGTAGTGGAAGGGTCTTT 8175  Qy 332LeuMetp 334  Db 8176 GCAGGACCCTTAGGTTGGGTCCATCCCCATGAGCACTTGTGTCGTTCACAGACCTCATGC 8235	7936 CGAGGACTITTCCAGCTATCACCTGTCTTCTTTACAACCTAGĠĀĀTĊCĀTCCTC  291 SCYSLeuAlaĀrgĀspProĀlaĀrgĀrgProSerĀlaHiSSerLeuLeuPheHiSĀrgVa	286	286	Qy 244 ABPIlePheSerPheGlyMetCyBAlaLeuGlu
9313 GAGACCATTTACCATCTTTGGGTCTCTGCTGCTCCTTCTGGGCTCCTCTGTAAAGCCGTG 430	Db 9193 CTCCCCCATCCCCTCTCTGGCATTGTATTCATCATCATCAGGACCCAAACCGAAGGCTGTCT 9252  Qy 429 429  Db 9253 TGGAAGCTTCCCTAATACTCAGGGCTGGTGCAGTAAGACGTGCTTTTCCGACTTCCCTTG 9312  Qy 429 429	429 9073 429 9133 9133	8893 AGTCCTTCCCCCATCCGGTTGCATGCTCTCTTCCAGAGGCTTTGGCTACGTCTGTTCCCC 429	Qy       429       429         Db       8713 GTGCTGTCTCTAGGAGTTGACCAATCAGGAAATGGAATGGATGCCTTTCTCTGGGGA 8772         Qy       429         Db       8773 CCCGCCTCTCCCCCATCCCCGTTCTCCCCCAGGCTGCCAGAGCCAAATCCAAGCTGACCC 8832         Qy       429         Db       8833 CTTTGTGGAAGCTGGAACCGGACCAAATCATTCCCCAGAGGCTTCTTGCTTTTAC 8892         Qy       429	Db 8415 CTAGGTACTCAGAGGTCTCCTTTGAGCTTGAACTAAATTCCTAGAGGATGT-CAGGTGA 8473  Qy 381

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                                                                                                                                                                                                                                                              RS Biren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Godd, S., Goyette, M., Grand-Pierre, N., Gard, S., Goyette, M., Grand-Pierre, N., Gardyna, S., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McLean, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Melman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rogetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Storawssh, M., Travers, M., Tradamas, J., Teefaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Submitted (10-FEB-2002) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 1 (bases 1 to 202844)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Anderson,S., Arachchi,H.M., Barra,N., Bastien,V., Bloom,T., Boguslawkiy,L., Boukbgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 202844)
Birren,B., Nusbaum,C. and Lander,E.
Birren,B., Nusbaum,C. and Lander,E.
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All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Submitted (05-00T-2004) Whitehead Institute/MIT Center for Genome Submitted, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: L20862
Center clone name: 192_B_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@broad.mit_edu
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                                                                                                     /rpt_family="B1_MM" 7176. .7216
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                            20331 CCCATACCGTTGATTGGCCCCACAACCATCCTTTTCCCCCAGGAGAAGATCCAGACCATG 20272
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91 PheGluGlnLeuValLeuValAspHisProAsnIleValLysLeuHisLysTyrTrpLeu 110
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                                                                                                                                           SerThrPheLeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHis 73
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                                                                                                       PheGlyAspArgLysAlaPheAlaAlaHisGlu---------
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244 AspIlePheSerPheGlyMetCysAlaLeuGlu 254	236		Pro11eArgAlaGluArgGluGluLeuArgAsnLeuHisPhePhePhe	GTGTGGGGACCATGGAGAACTTGTCTGTTTAGCTCCACCCTTTTCCTCAGCACTTCCTG	194 201	GGGAGCCCTGGACAG	190 BILEGIYSET	170 olleileHi9GlyAsnLeuThrSerAspThrIlePheIleGlnHi8AsnGlyLeuIleLy 190 	CCGGTTCTTCCTGCCTCTCATCCTCTATGCTTGCAGTTTTTTGCACGCCTGCAGTCCCCC	19792 AGAGCCTGGCCTTGCCCACGCGCTTGCCCCCTGCTCTGCACCTTTCCGCTGCTCTCTGAC 19733		149 AlaTrpLysArgTrpCysThrGlnIleLeuSerAlaLeu 161	19912 GTGGGGTAGCGGGCTCCCCCAGGCTCAGCCAGCCTTTTGGTGCCCCACCCGACGGAGTC 19853	GTCCAGCAGAACTTAGGGACAGTAGTGGGGGGGGGGGGACTCCGAAAAACCTTCGGTTCAGGA	20032 AAGAAGAACCACAAGGCCATGAACGCCCGGGTATGGGGAGTGGGCTTGGGGACTGGAGGGA 19973 148 148	139 LysLysAsnHisLysAlaMetAsnAlaArg	119 ValllePhelleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThr 138 	116	20211 GACGCCTCTGAGGC-CCGCGCGAGGGTGAAGCTAGGGGCGGGTGAAGGGCGGAGTGAAGCC 20153	
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stry: Dye-terminator Big Dye;	GAAG
Center project name: ACC	
Web site: http://www.hpcgg.org/Sequence/mouse.html Contact: hpgc@mendel.mgh.harvard.edu	CICIGIGGCIAAIACACCIICCCIGCCCACAGGIGGICCAGAIGCAGIGCAACCIIGAAAA I
Center: Harvard Partners Genome Center Center Code: HPGC	
On Sep	17216 GAGACCATTTACCATCTTTGGGTCTCTGCTGCTCCTTCTGGGCTCCTCTGTAAAGCCCGTG 17157 COMMENT
Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, 02119, USA	429 429
t Submission - State of Control of Control for	17276 TGGAAGCTTCCCTAATACTCAGGGCTGGTGCAGTAAGACGTGCTTTTCCCGACTTCCCTTG 17217
AUTHORS Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerant Ioshikhee, I.P., Shim, C., Decker, J., Thomas, E., Perera, A.,	429 429 AI
Bronx 3 (b	77
JOURNAL Submitted (15-ARR-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,	429
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Han, J	17456 CCTAAGCCCCAGCCTCCTGCTCCTCCTGGTGGCACCTTGGTTTTCTGTACAGTCACAC 17397 REF
TITLE High Throughput Mouse Sequencing TOTIONAL Hannihi shed	429 429 T
Inoxs ran, or, montgomery, s.i., sililb, s., wee, b., wong, o., romerantz, k., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon M. Goltz, I.S. and Kurbarlanatt D.	17516 CACCCTAAATTCAATTGCCAGTAGTCTACATGGCCTGCCCAGAGAACTAGTGGAAATCAG 17457
REFERENCE 1 (bases 13817)	429 429 REFI
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NISM Mus m	429 429 ORGA
N AC051	17636 AGTCCTTCCCCCATCCGGTTGCATGCTCTCTTCCAGAGGCTTTGGCTACGTCTGTTCCCC 17577  VERK
SEQUENCE, 46 unordered pieces. AC051615	429
AC051615 ITION Mus musculus strain C5	37
11 15	429
16678 TAGCAGCCTTTCTGGAGACCACTTTTCTCAAGTACCGAGGGACGCAAGCG 16629	CCCGCCTCTCCCCATCCCCGTTCTCCCCCAGGCTGCCAGAGACCAAATCCCAAGCTGACCC
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486AspAspArgMetLysL	420 A20 A20 A20 A20 A20 A20 A20 A20 A20 A
16797 ATGGCTTCCTGCACGA-GGTGGGCGGGTGCGCTTTGGGTGTGGAAAGGTGCAGGGTCTGC	416 roThrProGluProPheAspSerGluThrArgLysVallle
TGT	396 roLeuGlyLeuProArgValLeuAlaProProProGluGluValGlnLy8AlaLy8ThrP 416
16917 CTGGTAGTGGGGTCAGGTGGGTGGGCTGAGGCTCAGGCACTGGCTAGTGCCATGACTCATT	CCCCCTTGTCTATCCCCAGGAACGGGATCTATCCACTGATGAACTTTGCGGCTGCTCGGC
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449 euLeuValLeuGluAspArgLeuHisArgGlnLeuThrTyrAspLeuLeuProThr	ביריכי אתריכו את הייני ביריכי

Estimated insert size: agarose-FP - N/A

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Quality coverage: agarose-FP - N/A
Quality coverage: 6.8 x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is
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6: gap of unknown length
8: contig of 592 bp in length
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5: contig of 697 bp in length
5: contig of 697 bp in length
4: contig of 379 bp in length
7: contig of 313 bp in length
7: contig of 813 bp in length
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9: contig of 1882 bp in length
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of 727 bp in length
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of 1239 bp in length
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213817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap or contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of unknown length
g of 269 bp in length
of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        f unknown length.
g of 328 bp in length
""nknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      f unknown length
g of 1047 bp in length
f unknown length
g of 507 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            f unknown length
g of 374 bp in length
f unknown length
g of 174 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 536 bp in lounknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
of 1042 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown lengt
of 405 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 556 bp in length unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 1109 bp in 1 unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
of 260 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown length
of 511 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
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Qy 74 PheGlyAspArgLysAlaPheAlaAlaHisGlu	Db 13391 CGTATCAGGACACACTTCCTCCCACCTAGGTGAACCAAGGGAACATGCCCGGGATCCAG 13450  Qy 54 SerThrPheLeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHis 73	13271 TGGGTTCTTGATTCCCAGCCTTACCTCCTCAGCCCTCCCACTGAGCTGGGCAAGGCTAGC  44	QY 44 44  Db 13211 CCCAACCTCTAAAACCTGCGTACCTTCTGGCCCAGCCCCTGGACACCACCCTTCTCCCCC 13270  QY 44	Db 13091 GGCCCTCGGATCCCTTTGGCCCCAAGCCCTGGTGAGAAACCCCCATTCCTTGAACACCGG 13150  Qy 44	QY 44	12912 GAGAĞCĞAĞĞAĞĞĞĞĞAĞAĞĞĞĞTĞĞĞĞĞĞĞĞĞĞĞĞĞĞĞĞ	1 MetAlaAlaProGluProAlaProArgArgAlaArgGluCluArgGluCluA	/estimated_length=unknown
14589 CACCAGAGTATGGCGGTGAGTCCCTGAGCTGCTCTCAGGCATCTGACGGGCTAGCACATC  236	Db 14469 GTGTGGGGACCATGGAGAAACTTGTCTGTTTAGCTCCACCCTTTTCCTCAGCACTTCCTG 14528  Qy 211 spasplewargSerProIleArgAlaGlwargGlwGlwLewargAsmLewHisphePheP 231	14349 GGGAGCCCTGGACAGAGACTGCCCAGTCTCCCCGCCCAACTGACATCCTGTCTTTCTCTCC  194ValTrpHisArgIlePheSerAsn	Oy 190 811eGlySer	170 olleileHisGlyAsnLeuThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLy 	Db 14109 AGAGCCTGGCCTTGCCCACGCGCTTGCCCCTGCTCTGCACCTTTCCGCTGCTCTCTGAC 14168  Qy 162	149AlaTrpLysArgTrpCysThrGlnIleLeuSerAlaLeu	Oy 148	111 AspThrSerGluAla

449 euLeuValLeuGluAspArgLeuHisArgGlnLeuThrTyrAspLeuLeuProThr 467	381	Ş
446	QY       366TyrSerGluValSerPheMetGluLeuAspLysPheLeuGluAspVal 381       QY	부 <i>9</i>
437 rgSerGluAspLysAlaArgTrpHis	QY 365 365  Db 15727 CCTTCCTAGCTGGCTAGGCTTTGCCCTGACATCTCTCATGTACCTTTCCACACCATT 15786  Db	p 9
16745 CTCTGTGGCTAATACACCTTCCCTGCCCACAGGTGGTCCAGATGCAGTGCAACCTGGAAA 16804	QY 354 euProArgProArgProProLeuGlnTrpArg	B 9
GAGACCATTTACCATCTTTGGGTCTCTGCTGCTCCTTCTGGGCTCCTCTGTAAAGCCGTG	Oy 334 rOG1uAsnValValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluL 354	p 9
16625 TGGAAGCTTCCCTAATACTCAGGGCTGGTGCAGTAAGACGTGCTTTTCCGACTTCCCTTG 16684	15548 GCAGGACCCTTAGGTTGGGTCCATCCCCATGAGGACTTGTGTCGTTCACAGACCTCATGC 15607	무성
16565 CTCCCCCATCCCCTCTGGCATTGTATTCATCATTCAGGACCCAAACCGAAGGCTGTCT 16624	Db 15488 TGAGGGGCAGAAGGGCCGGGGTGGGTCAGGATCCTGGGGTCAGGTAGTGGAAGGGTCTTT 15547  Ov 332	δä
429 429	331 yr 331	ð
CTGCGGGGCACAGCGTTTCTTTGCTTTTCCACGGTTCTCTTTTCTGTTTTCTGTCTCTGC	OY 311	¦ ያ
16445 CCTAAGCCCCAGCCTGCCTGTCCTCCTGGTGGCACCTTGGTTTTCTGTACAGTCACAC 16504	15368 CTGCCTGGCCCGGACCCTGGCCGACACCCTCACACCCTCTTCCACCGACTA	뭐
429 429	291	9 9
16385 CACCCTAAATTCAATTGCCAGTAGTCTACATGGCCTGCCCAGAGAACTAGTGGAAATCAG 16444		2 S
429	15248 GTGGGAGGATGTGGTGATTGGACCGGTGGGGTCTAGAGTCTTGAAGGACCTCCTCTAGAG 15307	) <u>p</u>
16325 GTCTGGATCCAGAGCCATTGCTCCGGTCTCCCTTCTCATAGCTTCCTTTCGTTCCTAATA 16384	Qy 286 286 Db	9
AGTCCTTCCCCCATCCGGTTGCATGCTCTTCCAGAGGCTTTGGCTACGTCTGTTCCCC	Db 15188 CTGCTAATGGGATGACTTCTCTGCTCATTCATACAGGAAGGCTCTTTCAGCATCCCTGAG 15247	₽
429	286	9
16205 CTTTGTGGAAGCTGGAACCGGACCGACACAATCATTTCCCCCAGAGGCTTCTTGCTTTTAC 16264	15128 GCATACGTGTTTGGAGCCCAAGGCTTGCCTGTCCTCAAGTGTCCAGAATCAGATCTTGAG 1	뭐 !
429 429	286	9 !
CCCGCCTCTCCCCATCCCCGTTCTCCCCCAGGCTGCCAGAGACCAAATCCCAAGCTGACCC	286	į <u>9</u>
18085 GIGCIGICICIAGGAGITGACCACAAICAGGAAAIGGAAAIGGATGCCTTICICIGGGGA 16144	15	ᄗ
429	Oy 286 286 Oy	9
16026 CAACGCCAGAACCCTTTGACTCGGAGACCAGGAAGGTGAG-TCCCCACCTCCTGCTGTACT 16084	14948 TGCAGGTGCTTCAGCTTACCCTTGAAGTGCTCTAGGCAGGC	<b>p</b> :
416 roThrProGluProPheAspSerGluThrArgLysVallle 429	QY 286 286 QY	9 5
396 roleuglyLeubroArgValLeuAlaProProBroGlugluValGlnLysalaLysThrp 416	278 HisSerLeuSerAspProAsnMetArg2	; g
15906 CCCCCTTGTCTATCCCCAGGAACGGGATCTATCCACTGATGAACTTTGCGGCTGCTCGGC 15965	Qy         258 LeuGluIleGlnThrAsnGlyAspThrArgYslThrGluGluAlaIleAlaArgAlaArg 277         27         Y           Db         14828 CTCGAGATCCAAGCCAACGGGGATACCAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGG 14887         Db         Db         14828 CTCGAGATCCAAGCCAAGGAGTCACAGAAGAAGAGGCCATCGCTCGAGCCAGG 14887         Db         Db <td>₽ .S</td>	₽ .S
GAGCTGGCATGAGACTGAAGAAAAAGCACTATCAGGCCTGAGCCCCACCTAGCTACCCA	OY 255 Db 14768 TGCTCCAGGGTCTACGCCACCAATTCCAATTTGTCCCTGCACCCAGATGGCTGTA 14827	₽ <i>8</i>

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SOURCE
ORGANISM
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ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
Allen, C., Allen, H., Albbrooke, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baraber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Byrnt, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davyla, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Derson, S., Derson, S., Dunn, A., Durbin, K., Divyal, B., Eaves, K., Drager, H., Davyla, R., Durn, R., Durbin, K., Divyal, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fan, G., Chen, R., Garcia, A., Garra, M., Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guevara, W., Gue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17163 CGAGCTGCCCGGTACTACCATGCTTCCCTACTCATCCACTGCAGGATGACAGGACAAAGC 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17104 ATGGCTTCCTGCACGA-GGTGGGCGGGTGCGCTTTGGGTGTGGAAAGGTGCAGGGTCTGC 17162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17044 TGTCCTGTGTTCTCTCTCAGCGGACAGTGCCCAGGACCTCGCTGCTGAACTAGTGCATT 1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16925 TCTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCCAAG-TAGG 16983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus no
AC132640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muzny, D. Marie., Metzker, M. Lee., Abramzon, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC132640.3 GI:25007393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGCAGCCTTTCTGGAGACCACTTTTCTCAAGTACCGAGGGACGCAAGCG 17272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euAlaAlaPheLeuGluSerThrPheLeuLysTyrArgGlyThrGlnAla 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGTAGTGGGGTCAGGTGGTGGGCTGAGGCTCAGGCACTGGCTAGTGCCATGACTCATT 17043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 194709)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194709 bp DNA linear HTG 15-NG norvegicus clone CH230-339B14, WORKING DRAFT SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AspSerAlaGlnAspLeuAlaSerGluLeuValHisT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------AspaspargMetLysL 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG 15-NOV-2002
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced g1:23908481.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Warren,R., Wand,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Yakub,S., Yen,J., Yoon,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G., and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 194709)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (02-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 194709)
Rat Genome Sequencing Consortium
                                                                                        shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission

    Genome Center
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REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

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Center project name: KBQF
Center clone name: CH220-339B14
Center clone name: CH220-339B14
Center clone name: CH220-339B14
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 188047 bases at least Q40
Consensus quality: 189447 bases at least Q20
Consensus quality: 199412 bases at least Q20
Estimated insert size: 195068; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM Project Information

NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft\_dat. NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. data.html).

This sequence will be replaced is available and

by the finished sequence as soon as it the accession number will be preserved. 1 194709; contig of 194709 bp Location/Qualifiers

in length

1. .194709

FEATURES

/organism="Rattus norvegicus"
/mol\_type="genomic DNA"
/db\_xref="taxon:10116" /clone="CH230-339B14"

misc\_feature

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72 LeuHisPheGlyAspArgLysAlaPheAlaAlaHisGlu	52 LeuGlnSerThrPheLeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGlu 71 :::	45	GCTAGCAACACTTCATGGCTGGGGAAGGTTGTGGCAGAGACCACGTCCACACCCTGGG 54823	54942 CCCCTGGGTCATAGATTCCCCCAGCCTTACCTTCCCCAGCTTTCCCCACTGAGTTGGGCAGG 54883  QY	44 44 Oy	55002 TCCCCAACCTCTAAAACCTGCTTTACCTTCTGGCCCAGCCCCTGGACACCACCCCTCTTC 54943	55062 TGTCATCCCGGGACCACATCCACGTGCCTCTTGGATGCCCCACTACCCCTCTGGGTATAG 55003 OV	44	2 GGCCCTCGGATCCCTTTGGCCCCAAGCCCTGGTGAGAAACCCCCAAACCTTGAACACCAG	44	55182 CCATGGCATCCGAGAGGCCGAGCCAGTATGAGGGTCTCCCCGGACGCCTCTCTGGCCTTCTCGGA 55123	CGGGAGCAGGT-GGGCACGGTAACGCCACCGTCCCGTAGCCTAAGCATGGAGG 5		21 GIUSETGIUMSDGIUSETABDIIELEUGIUGIUSETPTOCYBGIYATGTTDGIILIYBATG 40	ייייייייייייייייייייייייייייייייייייי	gGluArgGluArgGluAsp 2	-618-941-99 (1-507) x AC132640 (1-194709)	Match: 58.26% Indels: 1036 14 Gaps: 18	Oy. NO.: 7.18e-121 Length: 194709 Oy. 1555.50 Matches: 468 31.32* Conservative: 13 Local Similarity: 30.47* Mismarches: 24	Scores:		misc_feature complement(191365192203)  /note="clone_boundary clone_end:Sp6	clone_end:T7	ion	-
228 HisPhePheProProGluTyrGly	Alaleuroaspaspleuargastrolieargalagiuargalugiuleuargaspleu 	GGTCTCTGGGGTGTGGGAGAAACTGGTCTCAGCATCACACTTTTTCTTA	CTCTTCTCTCTGGGCGGCGGTTGCAGTGTGGTACCGCATCTTCTCTAATGGTGTGTGT	194	193		186 snGlyLeuIleIysIleGlySer	166 laCysSerProProIleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHisA	54044 GGTGCGCTCTGACCCGGTTTTTCCTGCCTCCCTTCCTCTATGCTTGCAGTTTTTTTGCACG 53985	161Leu-SerPheLeuHiBA 166	54104 CAGGIGAGAGCCIGGCITGCCCACGCACTIGCCCCCIGCTCTTCCTTCACCTITCTTTCC 54045		149	TCAGGAGTGGGGTAGCGGGCGGGCTCCGCAGGCTCAGCCGCTCTTGGTGCCCACCCGAC	148 148	148 54284 GAGGGAGTCCAGCAGAACTTAGGGACAGTAGTGGGGCGGGGGACTCCGAGAGAGGCCTCGGT 54225	AGACCAAGAACCACAAGGCCATGAACGCCCGGGTATGGGGAGTGGGTTGGGGACTG	137 LysThrLysLysAsnHisLysAlaMetAsnAlaArg	117 AlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys 136 :::	54464 GAAGCCACAGGCTGGGTGGGCAGCATGGGGACCCCACCCGCAACGGCGGAGCCCGCCTGC 54405	116Cyp 116	109 TrpLeuAspThrSerGluAla	54583 ACCATGTTTGAGCAGCTGGTGGACCACCCCAACATCGTCAAGCTGCACAAGTAT 54524	TTTTGCCCTATACCGTTGATTGCCCCCACGACCATCCTTCTTCTCCAGGAGAAGATCCAG	

Db 51406 ACCTCAGGGATGGTGCAGTAAGATGTGTTTTCCGGACTTCCCTTGGAGATGTCTACCATT 51347	52486 GGCTAGGCTTTGGCTTGATGCCTCTTATGTCTTATGACACCTCTTCCATACCATCCCAGG 5
Qy 427 427	365
Db 51466 CATTGTATTCATCATTCAGTACCCAACAGAAGGCTACTACTCTTGGAAGCCTTCCCTAAT 51407	52545 GGACCCCAATGCAGTGGCG-GTGAGTGGTGGCAAATGAGGCTTCCCCTCCTAACTGCTT
Qy 427 427	359 ArabrobroLeuGlaTrnAra
Db 51526 GICTCIGCCTCICTGIGIGIGICTCIGICTCICCTCIGICCCTCTCICCCTCIGG 51467	52605 GAGGAAAAGACCAAGGCCATGGACTCCATGCAGTGTTTGGCTTGAGATGCCCCAGCCCCAT
Qy 427 427	339 GluGluLvsThrLvsAlaMetAspLeuHisAlaValLeuAlaGluLeuProArgProArg
Db 51586 TGCTTTCCACAGTTCTCTTTCTCTGTCTCTGTCTCGCTGTCTGT	THE LEWIS TO A TOTAL OF THE PROPERTY OF THE PR
Qy 427 427	38. [AV] [AVINACIONALITIES   AVINACIONALITIES   AVINACIONALITIES   AVINACIONALITIES   AVINACIONALITIES   AVINACIONALITIES
Db 51646 CCTGCTCCTGGTGGCACCCCATTTTTCTGTACTGTTGCACCCTGAGACACAGCATTTCCT 51587	SO KALLAJO U ROSTA LOLILILAZONO U ROLILAZONO LA CALENZO LA ROLILAZONO DE VINDAZO DE VIND
Qy 427 427	331
Db 51706 AAAAAAAAAAAAAGAAAAGAAAAAGAAAAAGAAAAAGAAAA	
Qy 427 427	316 jagarianivalanianhalaHisfyaDhallaGlnHisGln-Tvr 331
Db 51766 TAGGAAGCGTAAGGCCCTGGGTTGGGTCCCCAGCTCCGAAAAAAAA	52845 ACCONGCCGACCONAGCCCACAAACCTCCTCTTCCACCGACTGCTTTTGACCTGC 52786
Qy 427 427	206 gnDroàladrgaraProgaralaHigggerieniGnDhoHigaraVallenoDhoGluValH 316
Db 51826 GAGCTAGTAGAAATCAGCCTCAGGGGGTTTGGGGATTTTAGCTCAGTGGTAGAGCGCTTGCC 51767	ACCOACCACTACTTTCTTCCCACACACACACTTCATCCTCCTCC
Qy 427 427	287GlupheIleLeuCvsCvsLeuAlaArgA 296
Db 51886 TCAGCACACTAAATTCAAATGCCAGTCGTCTACATGTCCTGGATCCCAGCTGCACAGA 51827	AATGATTGGACCCGTGGGGTCTAGGGTCTTGAAAGATCTCCTCTAGAGCGAGGATTTTCC
Oy 427 427	
Db 51946 TTCCCCATCTGGATCCAGAGCCATCACTCTGATCTCCCCCATCCTAGCTTCCATCCTTCC 51887	b 53025 AATGGGATGCCTTCTCAGGCAGGCATGATGGAGGACATCATTGTGGAGGTGGGAGGATGC 52966
44.77	286 286
52006 TTTTACAGTCCTTCCCCATCCCATTGCGTGGTCTCTTCCATAGGCTTTTTGGCCACCTCCA	53085 GGTGTTTGGAGCCCAAGGCCTTCCTGCCCTCAAGTTTACAGAATCAGATCCTGAGCTGCT 53026
427	у 286 286
22/00 CICCCCMSGCIICCMSACCCMAAICCMAGCIGACCAIIIIICCCCMSAGGCIICIIGC	53145 AAAGGAAGACTCTTCTAGGAGCTCACGGAATTTCAAGAGGGTGAATGGAAGTAGGGCATG 53086
	286 286
52126 AGAGTTAACCACAACCAGGGAATGGGTGCCTCTGGGGACCTGTCTCTGTCCCAATT	53205 GGTCAGTACATTTGAAAGTGTTAGCATCTGAAAGCGTAGCTGGCGGACTGAGGTCACCTC 53146
242	у 286 286
52186 CCCTTTGACTCGGAGACCAGGAAGGTGAGTCCCAACTCCTGCTGTACTATGCTGTTTCTC	53265 ACTGGCTGCAGGTCTTGGGCCTTGAAGCCCTCTAGGTAGG
420 ProPheAspSerGluThrArgLys	
CCTCGTGTGTTGGCCCCACCCCCAGAGGAGGCCCAAAAGGCCAAAACTCCAACCCCCAGAA	b 53325 TCGGGCCAGCTCGCTGAGTGACCCCAACATGCGGGTGAGCAGCTTAACCCCTCTAGG 53266
Qy 400 ProArgValLeuAlaProProProGluGluValGlnLysAlaLysThrProThrProGlu 419	274 ABTTB ABTRH 650T 61050TBGDTDTDBGNM6TBTR
52306 ATCTCCAGGAATGGCATCTATCCACTCATGAATTTCGCTGCTCTGCGCCCTTGGGACTT	y 255 -MetalaValLeuGluIleGlnThrAsnGl
382ArgAsnGlyIleTyrProLeuMetAsnPheAlaAlaThrArgProLeuGlyLeu	TCATAGCCTCTGCTTTGGCTCTACTCCATCTCACCATTTCCAATTTGTGCCCTGCACCCA
52366 GCATGACAGTGAAGAAAAAACACTATCAGACCCGAGTCCCCACCTACCCTACCCCTGTCT	254 254
Db 52426 TACTCAGAGGTTTCCTTCGAGGTTGGACAAATTCCTAGAGGATGTCAGGTGAGAGCTG 52367	53504 GACTGCTGTGGACATCTTCTCCTTTGGGATGTGTGCACTGGA-GGTACTGTTCACTCTCC 53446
366 TyrSerGluValSerPheMetGluLeuAspLysPheLeuGluAspVal	YThralaValAspIlePheSerPheGlyMetCysAlaLeuGlu
	53564 GCACATCAGAATGTCCAATCAACTCTGCCTTGTTTTTCCCATTTCAGAGGTCAACGATGG 53505

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RESULT 13
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Allen, C., Allen, H., Albbrocke, S., Amin, A., Angulano, D., Anvalebechi, V., Aoyagi, A., Ayodeji, M., Bara, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Cheveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisl, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Havlak, P., Hamailton, C., Hamilton, K., Harnandez, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50986 CAGCCGACAGTGCCCAGGACCTCGCCGCAACTAGTGCACTATGGCTTCCTGCACGAGG 50927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 248568)

Matrice Matrice., Abramzon, S., Adams, C., Alder, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrPheLeuLyeTyrArgGlyThrGlnAla 507
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D, WORKING DRAFT SEQUENCE, 4
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Hollins, B., Howells, S., Hullyk, S., Hume, J., Idlebird, D., Jackson, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, W., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lux, Ma, J., Lewis, L., Liu, J., Loulseged, H., Lozado, R.J., Lux, Ma, J., Martin, K., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Milosavljevic, A., Miner, G., Minja, E., Monnemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Monnemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Monnemayor, J., Moore, S., Milosavljevic, A., Morris, S., Munidasa, M., Murphy, M., Nair, L., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Morgan, M., Morris, S., Milosavljevic, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasternak, S., Polindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sned, A., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Sovery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Sovery, R., Wolley, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Walter, B., Wang, J., Walter, B., Wang, J., Walter, P., Wang, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, S., Dunn, D., von, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Suth, A., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
of Molecular and Human Geneme Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 6, 2002 this sequence version replaced gi:23267220. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 248568)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 248568)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat Genome Sequencing Consortium.
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REFERENCE AUTHORS TITLE

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COMMENT

Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ -- Genome Center College of Medicine

Center project name: GSCY
Center clone name: CH230-52N10
Center clone name: CH230-52N10
Center clone name: CH230-52N10
Consensus quality: 230402 bases at least Q40
Consensus quality: 230402 bases at least Q30
Consensus quality: 234313 bases at least Q20
Batimated insert size: 237322; sum-of-contisting cartiers
Consensus quality: CH2602 bases at least Q20
Consensus quality: CH2602 bases at least Q30
CONSENSUS CH2602 bases CH2602 b Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

Qy         1 MetAlaAlaProGluProAlaProArgAlaArgGluGluGluGluGluGluGluGluGluGluGluGluGluG	Alignment Scores:  Pred. No.:  9.84e-121 Length:  Score:  1555.50 Matches:  468  Percent Similarity:  31.32% Conservative:  Best Local Similarity:  30.47% Mismatches:  Query Match:  14 Gaps:  US-10-618-941-99 (1-507) x AC115184 (1-248568)		feature	isc_feature	/organism="Rattus norvegicus" /mol type="genomic DNA" /db_xref="taxon:10116" /clone="CH230-52N10" misc_feature 11605 /note="wgs end extension clone_end:Sp6" misc_feature 49046845	ngth in le in le ngth in le in le	* NOTE: Estimated insert size may differ from sequence length  (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).  * NOTE: This is a 'working draft' sequence. It currently  * consists of 4 contigs. The true order of the pieces  * is not known and their order in this sequence record is  * arbitrary. Gaps between the contigs are represented as  * runs of N, but the exact sizes of the gaps are unknown.  * This record will be updated with the finished sequence  * as soon as it is available and the accession number will  * be preserved.  * 241125; contig of 241125 bp in length
Db 86694 GAGGGAGTCCAGCAGAACTTAGGGACAGTAGTGGGGGGGG	117 AlaArgValIlePhelleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys :::	Qy       109 TrpLewAspThrSerGluAla       115         Db	Qy 85	Qy 52 LeuGlnSerThrPheLeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGlu 71 :::	Qy         44	Qy       44       44       44         Db       85976       TCCCCCAACCTCTAAAACCTGCTTTACCTTCTGGCCCAGCCCCTGGACACCACCCCTCTTC       86035         Qy       44	Db 85796 CCATGGCATCCGAGAGGCCGAGCCAGTATGAGGGTCTCCCCGGACGCTCTGGCCTCTGGA 85855  Qy 44

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89032 TTCCCCATCTGGATCCAGAGCCATCACTCTGATCTCCCCCATCCTAGCTTCCATCCTTCC 89091	B7953 AATGGGATGCCTTCTCAGGCAGGCATGATGGAGGACATCATTGTGGAGGTGGGAGGATGC 88012
7	286
88972 TTTTACAGTCCTTCCCCATCCCATTGCGTGGTCTCTTCCATAGGCTTTTGGCCACCTCCA 89031	b 87893 GGTGTTTGGAGCCCAAGGCCTTCCTGCCCTCAAGTTTACAGAATCAGAATCCTGAGCTGCT 87952
427 427	286
88912 CTCCCCCAGGCTTCCAGAGACCAAATCCAAGCTGACCATTTTTCCCCCAGAGGCTTCTTGC 88971	87
427 427	V 286
88852 AGAGTTAACCACAACCAGGGAATGGGTGCCTCTGGGGACCTGTCTCTGTCCATCCCAATT 88911	286
CCCTTTGACTCGGAGACCAGGAAAGGTGAGTCCCAACTCCTGCTGTACTATGCTGTTTCTC	ACTGGCTGCAGGTCTTGGGCTTGCCCTTGAAGCCCTCTAGGTAGG
420 ProPheAspSerGluThrArgLys427	286
400 ProArgValLeuAlaProProProGluGluValGlnLysAlaLysThrProThrProGlu 419 	274
<b>&gt;</b>	255 -MetAlaValLeuGluIleGlnThrAsnGlyAspThrArgValThrGluGluAlaIleAl 274
GCATGACAGTGAAGAAAAAAACACTATCAGACCCGAGTCCCCACCTACCCTACCCTACCCTGTCT	Db 87533 TCATAGCCTCTGCTTTGGCTCTACTCCATCTCACCATTTCCAATTTGTGCCCCTGCACCCA 87592
381 381	
88552 TACTCAGAGGTTTCCTTGGAGCTGGACAAATTCCTAGAGGATGTCAGGTGAGAGCTG 88611	7 240 YThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGlu 254
GGCTAGGCTTTGGCTTGATGCCTCTTATGTCTTATGACACCTCTTCCATACCATCCCAGG	GCACATCAGAATGTCCAATCAACTCTGCCTTGTTTTTCCCCATTTCAGAGGTCAACGATGG 87473
365 365	236
359 ArgProproLeuGINTPARG	\frac{Qy}{228 HisPhePheProProGluTyrGly
GAGGAAAAGACCAGGGCCATGGACCTCCATGCAGTGTTGGCTGAGATGCCCCAGCCCCAT	GACTTCCTGACGATCTCCGGAGCCCTATAAGAACTGAACGGGAGGAGCTCCGAAACCTG 87353
	87293
332	202
GCCGGGGTGGACCAGGATCCTGGGGTCAGATCATGGA	87174 CTCTTTCTCTGCGTCGGCCGTTGCAGTGTGGTACCGCATCTTCTCCAATGGTGTGTGG 87233
	GACGCCCT 87173
315 18SETLEULYSLEULEUALAA.AHISCYSPÄELIEGINHISGIN-TYF 331	193
ACCCTGCCCGCCGACCCTCAGCCCACAACCTCCTCTTCCACCGAGTGCTCTTTGAGGTGC	Db 87054 ATGGCCTCATCAAGATCGGCTCTGGTGCTGGCGAGGCGGGGGGGG
	88994 CCTGCAGTCCCCCCATCATCCACGGAAACCTGACCAGCGACACGATCTTCATTCA
287	166 laCysSerProProIleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHisA
AATGATTGGACCCGTGGGGTCTAGGGTCTTGA	86934 GGTGCGCTCTGACCCGGTTTTTCCTGCCTCCCTTCCTCTATGCTTGCAGTTTTTTGCACG 86993
286 286	b 86874 CAGGIGAGAGCCIGGCIIGCCCACGCACIIGCCCCCTGCICTICCIICCACCIITCTITCC 86933 Qy 161

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   ThrPheLeuLysTyrArgGlyThrGlnAla 507
                                                                                                                                                                             TGGGCGGGTGCGCCTCGGGTTTGGAAAGGTGCAGTCTGCCGAGCTGCCCAGTACTACCGT
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                                                                                                          -AspAspArgMetLysLeuAlaAlaPheLeuGluSer
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RS Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lux, Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Direct Submission

Submitted (23-JUN-2004) National Institutes of Health, Xe Collection (XGC), National Institute of Child Health and Development, 6100 Executive Boulevard, Room 4B01, Rockvil
                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLILI at: http://image.llnl.gov Series: IRAK Plate: 130 Row: o Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: DOE Joint Genome Institute, Walnut Creek,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project
Contact: XGC help desk
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus tropicalis
Xenopus tropicalis
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                                                                                                                                               /organism="Yenopus tropicalis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www.jgi.doe.gov
note="Vector: pCMV-SPORT6.1"
                                                                                                                tissue_type="Embryo, Silurana
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                                                                                                                                                 AsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGlnIleLeuSerAla
                                                                                                                                                                                                                                                                                                                                                                   GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg
                                 IlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArgIlePheSer
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                                                                                        LeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeuThrSerAspThr
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                                                                                                                                                                                                                                                                                                           AAAATGCAGGAGGAGAAGTGAAAGCCGTGTTTGATAATCTTATCCAGCTGGAGCATCTT
                                                                                                                                                                                                                                                                                                                                   AlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuValAspHisPro
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/protein id="nuclear receptor binding protein"
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DESBILEESPCGRWQKRREEVWQRUVPGIDSALKAMDTEEGVEVWNNEVQPSERKNFK
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KNHKTMNEKANEWCTQILSALSYLHSCDPFIHGNLTCDTIFIQHNGLIKIGSVAPD
TINNHVKTCREEQKNLHFFAPEYGEVTMVTTAVDIYSFGMCALEMAVLEIQGNESSY
VPQEAINNAIQFLEDPLQREFIQKCLETDPSKRPTARELLFHPALFEVPSIKILAAHC
IVGHQHMIPENALEEMTKNLDMSAVLAEISHADREGVENIFSQSPALELDKFLEDVRN
GIYPLTAFGVPRPQQPQQEVVKSPVVPPSVKTPTPEPAEVETRKVVQMQCNIESVDEG
AKHHITLLLKLEDKLANHLSCDLLPNENIQELAABELVQLGFVSBSDQIRLACLLEEAF
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BC004756 2128 bp mRNA line
Mus musculus nuclear receptor binding protein,
MGC:6961 IMAGE:3154089), complete cds.
BC004756
BC004756.1 GI:13435803
MGC.
MGC musculus (house mouse)
                                                                                                                                                                                                                                                            GCCTGTTTACTTGAAGAAGCTTTCAGCAAGTTC
                                                                                                                                                                     AlaAlaPheLeuGluSerThrPheLeuLysTyr 502
                                                                                                                                                                                                     GAGCTGGCAGCAGAGCTGGTACAGTTGGGCTTTGTCAGTGAGTCCGACCAGATTCGACTC
                                                                                                                                                                                                                       AspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAspArgMetLysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: a Column: 1
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Den, CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                    clone was selected for full length sequencing because it
ed the following selection criteria: matched mRNA gi: 22219433
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natl. Acad. Sci.
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Search completed: January 13, 2006, 23:36:28 Job time : 6726 secs

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Sequence:
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Sequence 1053, Ap
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Sequence 9, Appli
Sequence 69, Appl
Sequence 1428, Ap
Sequence 9, Appl
Sequence 9, Appl
Sequence 1339, Ap
Sequence 13370, A
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## ALIGNMENTS

RESULT 1 US-09-976-594-1053

Sequence 1053, Application US/09976594 Patent No. 6673549

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GENERAL INFORMATION:

APPLICANT: Furness, Michael

APPLICANT: Buchbinder, Jenny

APPLICANT: Buchbinder, Jenny

ITILE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREE

FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240,409

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143

SOPTWARE: PERL Program

SEQ ID NO 1053

LENGTH: 4048
US-10-618-941-99 (1-507) x US-09-976-594-1053 (1-4048)
                                                        Best Local Similarity:
Query Match:
                                                                                                                                     Pred. No.:
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                                                                                             Percent Similarity:
                                                                                                                                                                                           US-09-976-594-1053
                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                             FEATURE: NAME/KEY: misc_feature
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Matches:
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Sequence 9, Application US/09345473E
Patent No. 6558903
GENERAL INFORMATION:
APPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558903el Kinases and
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
SEQ ID NO
TYPE: DOA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1):...(981)
OTHER INFORMATION: n = A,T,C or G
US-09-345-473E-9
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: NO. 6858418el Kinases and FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                        Sequence 9, Application US/09862027
Patent No. 6858418
GENERAL INFORMATION:
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; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1).T.(981)
; OTHER INFORMATION: n=A,T
US-09-862-027-9
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Query Match:
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Pred. No.:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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LENGTH: 2029 base pair
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APPLICATION NUMBER:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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APPLICANT: Guegler, Karl J.
APPLICANT: COrley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
                                                No : :
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FILING DATE: September
CLASSIFICATION: 536
                                                                                                           LIBRARY: BRAI'
CLONE: 864683
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OPERATING SYSTEM:
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CITY: Palo Alto
                                                                                                                                                                                        TYPE: nucleic acid
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Hillman, Jennifer L
Bandman, Olga
Shah, Purvi
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                GAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAGTGCCGTACTGGCTGAAATC 1217
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                                   GluAsnValValGluCluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeu 354
                                                                                                      ValHisSerLeuLysLeuLeuAlaAlaHisCysPheIleGlnHisGlnTyrLeuMetPro
                                                                                                                                                                   ArgAspProAlaArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGlu
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RESULT 5
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Weil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
APPLICATION NUMBER: US/09/234,613
FILING DATE
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 9F-0356 US
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FABLESE for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
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CITY: Palo Alto
STATE: CA
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SEQUENCE CHARACTERISTICS:
LENGTH: 2029 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUTO3
CLONE: 864683
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                       AlaValLeuGluIleGlnThrAsnGlyAspThrArg---ValThrGluGluAlaIleAla
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                                                                     GTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGGCATGTGTGCACTGGAGATG
                                                                                          ValAlaAsp---GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet
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   GCAGTGCTGGAGATTCAGGGCAATGGAGAGTCCTCATATGTGCCACAGGAAGCCATCAGC
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; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1428
                                                              PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PELLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PELLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: VENTER,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1428, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                          APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                  TCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTTCCACCCAGCATTGTTTGAA
                                                                                                                                                                                                                                                                                                                                                 ValAlaAsp---GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet
                                                                                        ArgAspProAlaArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGlu 314
                                                                                                                                                    ArgAlaArgHisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAla 294
                                                                                                                                                                                                                                                              AlaValLeuGluIleGlnThrAsnGlyAspThrArg---ValThrGluGluAlaIleAla
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RESULT 7
US-09-023-942A-9
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Patent No. 6479274
GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Ton:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFICATION UMBER: PO5101/97
APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP0422/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP0422/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION NUMBER: INTERNATION:
APPLICATION NUMBER: INTERNATION:
NAME: DIGIGLIO, FRANK S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: (US only) ANTALIS Toni Marie
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
CORRESPONDENCE SCULLY, SCOTT, MURPHY & PRE
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: 110°
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Best Local Similarity:
Query Match:
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS;
LENGTH: 2241 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEPAX: (516) 742 4366
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LOCATION:
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TOPOLOGY: lin
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  ValAlaAsp----GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet
                                        GTGAAGACTTGTCGAGAAGAAGCAGAAATCTACACTTCTTTGCACCAGAGTATGGAGAA
                                                                           IleArgAlaGluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGlu
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                                                                                                                                                                                 Sequence 1939, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
                                             SEQ ID NO 1939
                                                     APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PAECENTIN Ver. 2.1
LENGTH: 2546
TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 9
US-09-949-016-13170
; Sequence 13170, Ap;
; Patent No. 6812339
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DB:
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR PRILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-09-08
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Matches:
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1 1	Qy 111 111  Db 7485 ATTGCAAAGAGACTAGCTACATTTATTATTGTTCCTTTTACACTCAGAGATTAAAACAAG 7544	Qy 109 pleuasp	Qy 89 rValPheGluGlnLeuValLeuValAspHisProAsnIleValLysLeuHisLysTyrTr 109       ::: :::::	7305 ACAGTGATTTGTGACTCTGTTATTCCACTGTCTCCCTTGCTTTCAGGAAAAGGTTCGTGC 7	Db 7245 GAGTATGTTGGGGTTAGATCGTTTCTGGGGAGGGATAGGGAATGGCTTCTCAGGATTATT 7304	Db 7185 GGGGAATGTTGGAACACTGATGTTAGAGAGGAATTGGTGTTGGGAAGCTGCCCGTGAGGA 7244  Qy 83 83	83	Qy 74 PheGlyAspArgLysAlaPhe-AlaAlaHis	Oy 54 SerThrPheLeuhlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHis 73      ::	7005	6945 TGGGGGCTAGGAGGAGTGATCATATGGAGTGTTAAAATGGAGGATTTGTGAGATAAGTT	Oy 42 42	6885 TGGAAAGGTGAGAACTGGAAGAGCAAAGTCTTAAAAGAGGCCAACCAA	42	Qy 37 TrpGlnLybArgArgGlu	67	17 Glubraglubergluberglubergluberdluserberlingerberlingluserbergragivava	3 Gaps: -618-941-99 (1-507) x US-09-949-016-13170 (1-176:	cal Similarity: 21.97% Mismatches: atch: 15.49% Indels:	d. No.: 7.3e-34 Length: re: 413.50 Matches: Conf. 5418 Concerns to the conf. of the	Alignment Scores:	) ORGANISM: Human US-09-949-016-13170	LEW 15 NO 131 / O   O   O   O   O   O   O   O   O   O	; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSEQ for Windows Version 4.0
RESULT 10 US-09-040-984-23 ; Sequence 23, Application US/09040984 ; Patent No. 6210883	Qy 185 isAsnGlyLeuIleLysIleGlySer 193	Db 8503 ACTCCTGTGACCCCCCCATCATCCATGGGAACCTGACCATCTTCATCCAGC 8562	8443 CCCCTGCCCTTAATTTCCCAGTGGCCCCTCTAACAGCCCAGTGCCCCCACAGCTACCTGC	8383 GATTATCTTTATGGTGACCAGCAGGAGACCTGGCCCTTGCTCCTCTTAAC	Db 8323 TCTCCTAGTGCTTATCCAGCTATTTAAATCATCAGGCATAATGGAGATTCAGAGTGTGGG 8382  Qy 161 161	161	Db 8263 ACGGGTCTTTAAAGGGTGCGTCCTAATGCCCTAACCACGACACTTATCTCCTACCTCTT 8322	8203 TGTTCTATTCTGCCTCTCCCCACTTTCTTTGAATCATATACTGTCAAGATTAGGGCCCCT	8143 GTTTCTTACCCATATTTCCTGATGTAGTTACTCCAAACAGATTTCAGGGCACTACTCTTC	Db 8083 GGCATGGAAGCGTTGGTGCACACAAATCCTCTCTGCCCTAAGGTAAGTAGTACCTGGTTA 8142  Qy 161 161	Qy 149 -AlaTrpLysArgTrpCysThrGlnIleLeuSerAlaLeu 161	148	7963 GGGGTGGTTTTAAAAAGGACTCTGTTAATAATGAAGCTGATCAGGAAGGGACGGAAGGAG	Qy 148 148	7904 CANGACGATGAATGA-AAAGGTATAGAAGGAGAGAGACAAAGTTTGAGGCTGGTTTTTG	Db 7844 CACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAAGAAGAAGAACCA 7903	Qy 122 eThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLysLysAsnHi 142	7784 GGGATCATTTCTACTATAAGGCCTTTTAGTAAGTGCTTTGCCTCCCCAGGTCATTTTAT	Oy 117Alahrdvahusakusakusakustittakokakustitokakatittakakatatustikakokakusakusakaka //83	116	Db 7665 CTTCCCATAACTTTCATT-GCTTGTTTTCATTGCCCTATTTAGTCTAAGTAAGGTAAAGCT 7723	Qy 112 ThrSerGluAlaCys 116	Db 7605 CACCTATGCCTTTTGTGTGGCTATAGATTGGGCAGAAAATGAGTGAACTTTTGCTTCTTT 7664	Qy 111 111

GENERAL INFORMATION:

Steven G.

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DB:
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Best Local Similarity:
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SOFTWARE: FASCESO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,984
FILING DATE: 18-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
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SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
TYPE: nucleic acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, TongTong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, APPLICANT: Wang,
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                                  GTCAAACACCACCTGACACTTCTGCTGAAGTTGGAGGACAAACTGAACCGGCACCTGAGC
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TyrAspLeuLeuProThrAspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGly 481
                                                      AlaArgTrpHisLeuThrLeuLeuValLeuGluAspArgLeuHisArgGlnLeuThr
                                                                                                                              AspSerGluThrArgLysValIleGlnMetGlnCysAsnLeuGluArgSerGluAspLys
                                                                                                                                                                                              GluGluVal------GlnLysAlaLysThrProThrProGluProPhe
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Query Match:
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APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FO
FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/040,802
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
COMPTAINE: DATE: 198-03-18
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US-09-123-912-23
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SEQ ID NO 23
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Patent No. 6312695
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OTHER INFORMATION: Where n
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                                                                 GTCAAACACCACCTGACACTTCTGCTGAAGTTGGAGGACAAACTGAACCGGCACCTGAGC
                                                                                                                                                             AspSerGluThrArgLysVallleGlnMetGlnCysAsnLeuGluArgSerGluAspLys
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APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FASESEQ for will
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US-09-643-597-23
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NAME/KEY: misc_feature
LOCATION: (1)...(669)
OTHER INFORMATION: n =
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TYPE: DNA
ORGANISM: Homo sapien
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Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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Bangur, Chaitanya S.
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LOCATION: (1)...(669)
OTHER INFORMATION: n =
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APPLICANT: Wang, Tongtong
APPLICANT: Hosken, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
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APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PROPERTY OF LUNG CAUTILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
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SEQ ID NO 23
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TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(669)
OTHER INFORMATION: n = I
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                                TTCATTAGTGAGGCTGACCAGAGCCGGTTGACTTCTCTGCTAGAAGAGAGACT
                                                                                                   TGTGACCTGATGCCAAATGAGAATATCCCCGAGTTGGCGGCTGAGCTGCAGCTGGCCTGGGC
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                                                               PheLeuHisGluAspAspArgMetLysLeuAlaAlaPheLeuGluSerThr 498
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CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 669
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GENERAL INFORMATION:
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya
APPLICANT: Hosken, Nancy
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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ORGANISM: Homo sapien
FEATURE:
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Fanger, Gary R
Li, Samuel X.
Wang, Aijun
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Matches:
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Search completed: January 14, 2006, 00:50:21 Job time : 275 secs

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GENERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: CAENEPEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: US/10/618,941
CURRENT FILING DATE: 2002-07-15
PRIOR FILING DATE: 2002-07-15
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INVERENT FILING DATE: 2002-07-15
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GENERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
CURRENT FILING DATE: 2003-07-15
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SOFTMARE: PAtentin version 3.2
SOFTMARE: PAtentin version 3.2
SEQ ID NO 99
LENGTH: 507
TYPE: PRT
ORGANISM: Homo sapiens
US-10-618-941-99
MAAPEPAERRAREREREDESEDESDILEESPCGRWQKRREQVNGGNMPGLQSTFLAMDTEEGV
EVWNELLFGDIKAFAAHEEKIOTVFEOLVLUDHPNIVKLHKYMLDTSERCARVIFITEVSSGS
LKQPLKKTKNHKAMNARAWKRWCTQILSALSFILHACSPPIHGNLTSDTIFIQHNGLIKIGSVW
HRIFSNALRPTALPDDLRSPIRAREELRNLHFFPPEVGLVALDTFECHMSLIKIGSVW
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FIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMN
PAATRPLGLFRVLAPPBEVGKAKTFTPEPFDSETRKVJOMCCNLERSEDKARWHLTLLLVLEDR
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Q5NUTZ7 XENLA
Q5SHB TETING
Q9NUY6 HUMAN
Q4RKP5 TETING
Q9NUY6 DROME
Q9Y0Y6 DROME
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Q9Y0Y6 DROME
Q9Y0Y6 TETING
Q9HUJ5 MOUSE
Q9Y0Y6 GRAEEL
Q8R3M0 MOUSE
Q5VP7 HUMAN
Q4F2 HUMAN
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Craniata glires;  636; DOI 64, Kiyosawa 71, Bon 71,	ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  PRT; 547 AA.  BLrel. 23, Created)  BLrel. 23, Last sequence upd  BLrel. 26, Last annotation u t male corpora quadrigemina clone:B230344L17 product:S1	QSJRC1_HUMAN QSJRC2_HUMAN QSJRCX6_HUMAN Q8JCX6_HUMAN Q6JP76_HUMAN Q6JP76_HUMAN Q6JCU2_XENLA Q9STK6_ARATH MNK4_RAT WNK4_RATH WNK4_RATH Q8SRY9_ARATH Q9SHV8_ARATH Q9SHV8_ARATH Q9SHV8_ORYSA
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A Havashida S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Ra Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Hori F., Imotani K., Sojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

A Katihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Ohsato N., Okazaki Y.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Satoh H., Sakoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

B Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO46142; BAC32612.1; -; mRNA.

EMBL; AKO46142; BAC32612.1; -; mRNA.
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Best Local S
Matches 310
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Genome Res.
[6]
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MEDLIND=20530913; pubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Kegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
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sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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Probom; Pb000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Nucleotide-binding;
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GO:0005524; F.ATP binding; IEA.
GO:0004672; F:protein kinase activity; IEA.
GO:0004872; F:receptor activity; IEA.
GO:0016740; F:transferase activity; IEA.
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                                                                                                                         KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH
                                                                                                                                                                                                                                        RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK
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                                            RIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVAD-GTAVDIFSFGMCALEM
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Hopkins R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schein J.E., Jones S.J.M., Marra M.A.,
Ra Generation and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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mitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

3L; BCO74684; AAH74684.1; -; mRNA.

GO:0005524; F:ATP binding; IEA.

GO:0004674; F:protein serine/threonine kinase activity;

GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO:0004872; F:receptor activity; IEA.

GO:00064872; F:protein amino acid phosphorylation; IEA.

GO:0006463; P:protein amino acid phosphorylation; IEA.

cerPro; IPR000719; Prot kinase.
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c. Natl. Acad. Sci. U.S.A.
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NUCLEOTIDE SEQUENCE.
STRAIN=129, and FVB/N,
STRAIN=129, and FVB/N,
STRAIN=129, and FVB/N,
TISSUE=Mammary tumor. Brcal-/fl, and Mammary tumor. C3;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Klauener R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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SEQUENCE
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01-JUN-2001 (TrEMBLrel. 17, Last
10-MAY-2005 (TrEMBLrel. 30, Last
Nuclear receptor binding protein
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SMART; SM00220; S_TKC;
SMART; SM00219; TyrKC;
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Eu
Muridae; Murinae; Mus
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Q99J45;
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                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Nrbp;
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AD Diatchenko L., Marusina K., Farmer A.A., Rubin-G.M., Hong L.,
AN Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
AN Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
AR Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
AN Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
AN Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
AN Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Whiting M., Ketteman J.W., Green E.D., Dickson M.C.,
AN Hiting M., Krzywinski M.I., Skalska U., Smailus D.E.,
AN Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences ",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 307
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A MCCUlloch R., Lim R., Ingley E., Williams J., Klinken S.P.

A MCCUlloch R., Lim R., Ingley E., Williams J., Klinken S.P.

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; BC004756; AAH04756.1; -; mRNA.

EMBL; BC018463; AAH18463.1; -; mRNA.

EMBL; AF302138; AAK97261.1; -; Genomic DNA.

R EMBL; AF302139; AAK97261.1; -; Genomic DNA.

R Ensembl; ENSMUSG00000029148; Mus musculus.

R GG; GG:0004572; F: Protein kinase activity; IEA.

R GG; GG:0004672; F: receptor activity; IEA.

R GG; GG:00046740; F: receptor activity; IEA.

R GG; GG:000
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MEDLINE-22287351; PubMed=12176995; DOI=10.1074/jbc.M206041200;

Lim R., Winteringham L.N., Williams J.H., McCulloch R.K., Ingl.

Tiao J.Y.-H., Lalonde J.P., Tsai S., Tilbrook P.A., Sun Y., Wu

Morris S.W., Klinken S.P.,

"MADM, a novel adaptor protein that mediates phosphorylation o

14-3-3 binding site of myeloid leukemia factor 1.";

J. Biol. Chem. 277:40997-41008(2002).
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                                                  RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADVKENKARVIFITEYMSSGSLKQFLK
                                                                                  RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK
                                                                                                                                                        BEEESEDESEILEESPCGRWQKRREEVNQRNVPGIDSAYLAMDIBEGVEVVWNEVQFSE
                                                                                                                                                                                EREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGD
  KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH
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61.5%;
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Pred. No. 1.7e-102;
B; Mismatches 105;
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ID Q8NCX 8 HU
Q8NCX 9 HU
Q8NCX 10 Q8NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl; ENSG00000185189; Homo sapiens.
HGNC: HGNC: 19339; NRBP2.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0004678; P:protein amino acid phosphoryll
InterPro; IER000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last samotation updat
Hypothetical protein DKFZp434I2411 (Fragment).
Name=NRBP2; Synonyme=DKFZp434I2411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bahr A., Lauber J., Mewes H.W., Weil B., Amid Han M., Wiemann S.; Submitted (SEP-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                             Hypothetical protein.
NON TER 1
SEQUENCE 294 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                Prodom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
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61
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                                ARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAHCFIQHQYLM
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                                                                                                   RSPIRAEREELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNGDTRVTEEAI
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ARARHSLSDPNMREFTLCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAHCFTQHQYLM
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                                                                                                                                                                                                                            Score 1536; DB 2; 1
Pred. No. 9.7e-103;
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                                                     RX PubMed=14702039, DOI=10.1038/ng1285;
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
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RA Gekine M., Obayashi M., Mishi T., Shibahara T., Tanaka T., Ishii S.,
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RA Sugawara Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
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RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y. Takiguchi S., Watanabe M., Hara H., Tanase T.-O.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matanabe T., Sugiyama A., Takemoto M., Kawakami B.,
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RA Matagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
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RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
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RA Mizushima Sugano J., Satoh T., Shigata K., Sasaki M.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RODAS T., Nakagawa K.,
RA, Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA Nakai K., Yada T., Nakagawa K.,
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RA, Nakaga M., Takama K.
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QSUHY1;
01-MAY-2000 (TremBLrel. 13, C
01-MAY-2000 (TremBLrel. 13, I
13-SEP-2005 (TremBLrel. 31, I
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MEDLINE=20304761; PubMed=10843813; DOI=10.1006/geno.2000.6167;
MEDLINE=20304761; PubMed=10843813; DOI=10.1006/geno.2000.6167;
Hooper J.D., Baker E., Ogbourne S.M., Sutherland G.R., Antalis T.I.
"Cloning of the cDNA and localization of the gene encoding human I
a ubiquitously expressed, multidomain putative adapter protein.";
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Multiple domain putative nuclear protein (Hypothetical protein
FLJ11084) (Hypothetical protein DKFZp564D1878) (Nuclear recepto
binding protein) (Hypothetical protein NRBP).
Name=BCON3, Synonyms=DKFZp564D1878, NRBP;
                                            CDNAS
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Mammalia; Eutheria;
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                         36:40-45(2004)
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RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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EMBL; AK001946; BAA91993.1; -; mRNA.
EMBL; AL136682; CAB66617.1; -; mRNA.
EMBL; BC001221; AAH01221.1; -; mRNA.
EMBL; BC001221; AAH01221.1; -; mRNA.
EMBL; BC001221; AAY14847-1; -; mRNA.
EMBL; BC0074117; AAY14847-1; -; mRNA.
EMBL; BC0074117; AAY14847-1; -; mRNA.
EMBL; BC00701015216; Homo sapiens.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0007165; P:sH3/SH2 adaptor activity; TA
Query Match 57.1
Best Local Similarity 61.0
Matches 305; Conservative
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Submitted
                                                                                                                      ProDom; PD000001; Prot kinase; 1.

PROSITE; P850011; PROTEIN_KINASE_DOM; 1.

ATP-binding; Hypothetical protein; Kinase; Nuclear protein; Nucleotide-binding; Receptor; Serine/threonine-protein kina
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Submitted (FEB-2002)
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Submitted (DEC-2000)
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Ottenwaelder B., Obermaier B.
Mewes H.W., Weil B., Amid C.,
                                                                                       Transferase.
SEQUENCE 535
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sapiens BAC clone RP11-413M20.";

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Score 1534.5; DB 2
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9; Mismatches 102;
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Query Match
Best Local :
                                                                                                                  Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.; "Substitution rate and structural divergence of 5' UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs."; Submitted (WAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB168327; BAE00451.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                            International consortium for macaque "DNA sequences of macaque genes expre evolutionary implications."; Submitted (JUN-2005) to the EMBL/GenE
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Testis cDNA clone: QtsA-11263, similar to human nuclear binding protein (NRBP) (Brain cDNA, clone: QnpA-17237, human nuclear receptor binding protein (NRBP),).
Macaca fascicularis (Crab eating macaque) (Cynomolgus mo
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Mammalia; Eutheria; Euarchontoglires; Primates;
Cercopithecidae; Cercopithecinae; Macaca.
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57.5%;
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Score 1534.5; DB 2
Pred. No. 2.7e-102;
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QSO OCC EPO OC
                                                                           A Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
A Fobo G., Han M., Wiemann S.;
L Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR858669; CAH90881.1; -; mRNA.

GO; GO:0005524; F:ATP binding; IEA.
R GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
R GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
R GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
R GO; GO:0016740; F:transferase activity; IEA.
R GO; GO:0016740; F:transferase activity; IEA.
R GO; GO:0016740; F:transferase activity; IEA.
R InterPro; IPR000719; Prot kinase.
R InterPro; IPR0007290; Ser_th_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Pfam; PF00069; Pkinase; I.
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SMART; S
SMART; S
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01-FEB-2005 (TrEMBLrel. 29, Last sequence up
01-FEB-2005 (TrEMBLrel. 29, Last annotation
Hypothetical protein DKFZp459G2032.
Name=DKFZp459G2032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
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The German cDN
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NCBI_TaxID=9600;
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; PD000001; Prot_kinase; 1.
SM00220; S_TKC; 1.
SM00219; TYrKC; 1.
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Matches 305
                                                                           Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical Name=NRBP;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-CCT-2003 (TrEMBLrel. 25, Last annotation
Hypothetical protein FLJ14632.
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Q96SU3;
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SEQUENCE 535 AA; 59818 MW; 398078
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NCBI_TaxID=9606;
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                               (xeno); NbExp=1;
8; BAB55185.1; -;
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Pred. No. 2.7e
59; Mismatches
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R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA

R GO; GO:0004674; F:transferase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0016740; F:protein amino acid phosphorylation; IEA.

R InterPro; IPR000719; Prot kinase.

R Pfam; PF00069; Pkinase; 1.

R ProDom; PD000001; Prot kinase; 1.

R PROSITE; PS50011; PROTEIN KINASE DOM; 1.

R PROSITE; PS50011; PROTEIN KINASE DOM; 1.

W ATP-binding; Kinase; Nucleotide-Dinding;

W Serine/threonine-protein kinase; Transferase.

SEQUENCE 535 AA; 59850 MW; 4829CA7CB60F0175 CRC64;
NUCLEOTIDE SEQUENCE.
TISSUE=Kidney;
Maruyama K., Sugano S
"Oligo-capping : a si
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25 HUMAN
Q53FZ5 HUMAN
Q53FZ5;
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Homo egilens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
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Nuclear receptor binding protein
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Suzuki Y., Sugano S., Totoki Y., Toyoda A., T
Tanaka A., Yokoyama S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ
EMBL; AKZ23136; BAD96856.1; -; mRNA.
HGNC; HGNC:7993; NRBP.
GO; GO:0005524; F.ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine ki
GO; GO:0004713; F:protein-tyrogine kinase act
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0006468; P:protein amino acid phosphor
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Gene 200:149-156(1997).
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I. Genome Biol. 6:R6-R6(2005).

R EMBL; AJ721116; CAG32775.1; -; mRNA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004674; F:pxotein serine/threonine kinase activity; IEA.

R GO; GO:0004713; F:pxotein-tyrosine kinase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R InterPro; IPR00719; Prot kinase.

InterPro; IPR002290; Ser_Ehr_pkinase.

R InterPro; IPR002291; Ser_Ehr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR0001245; Tyr_pkinase.

R Pfam; PF00069; Pkinase; I.

R Pfam; PF00069; Pkinase; I.

R Pfam; PF0001001; Protekinase; 1.

R SMART; SM00219; TyrKc; 1.

R SMART; SM00219; TyrKc; 1.

R Hypothetical protein.
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Hypothetical protein.
ORFNames=RCJMB04_35j18;
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J., Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M., Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.; "Full-length cDNAs from chicken bursal lymphocytes to facilitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CB; TISSUE=Bursa; Caldwell R.B., Kierzek A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPPEYGEVAD-GTAVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V$$G$LKQFLKKTKKNHKAMNARAWKKWCTQIL$AL$FLHAC$PFIIHGNLT$DTIFIQH
SEADQSRLTCLLEEAFSKFYYTR
                                        HEDDRMKLAAFLESTFLKYRGTQ 506
                                                                                                                                       ETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFL
                                                                                                                                                                                    MIFSQSPALELDKFLEDVRNGIYPLTAFGMPRPQQPQQVVVKSPIAPPSVKTPTPEPAEV
                                                                                                                                                                                                                                                                                RELLFHQALFEVPSLKLLAAHCIVGHQHMIPENALEEMTKNLDMSAVLAEINHADREGVK
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                                                                                           ETRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLQPNDNIQELAAELVQLGFI
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Pred. No. 3.6e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2176262D10AECE76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 124;
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QÉNTZY 111
QÉNTZY 26
QÉNTZ
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Wullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Witing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6NTZ7;
Q6NTZ7;
05-JUL-2004 ('05-JUL-2004 ('
                                                                     Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM002219; TYCKC; 1.
SMART; SM00219; TYCKC; 1.
SPROSITE; PS50011; PROTEIN KINASE DOM; 1.
SEQUENCE 526 AA; 59366 MW; E966F6C5FCBC742B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 Klein S., Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC068805; AAH68805.1; -; mRNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001648; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vej
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genetic and genomic tools initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _XENLA
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   56.7%;
58.8%;
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27,
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      Score 1514;
Pred. No. 8
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Craniata; Vertebrata; Euteleostomi;
esobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Хепорив
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                                    띪
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TO SHOW THE PROPERTY OF THE PR
                                                    Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; AL954831; CAIZ0617.; -; Genomic_DNA.

R GG; GG:0005524; F:ATP binding; IEA.

R GG; GG:0004674; F:protein serine/threonine kinase activity; IEA.

R GG; GG:00044713; F:protein-tyrosine kinase activity; IEA.

R GG; GG:0004872; F:receptor activity; IEA.

R GG; GG:0004878; F:protein amino acid phosphorylation; IEA.

R GG; GG:000466; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR0012290; Ser_Thr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; DPR0001; Prot_kinase.

R Pfam; PD000069; Pkinase; 1.

R PFAm; PD000069; Pkinase; 1.

R PFAm; PD0001; Prot_kinase; 1.

R SMART; SM00219; TyrKc; 1.
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NUCLEOTIDE
Phillimore
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01-FEB-2005
01-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSSNQ3_BRARE
Q5SNQ3;
                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=DKEY-12H9.7-001;
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(TrEMBLrel. 29, Last sequence update)
(TrEMBLrel. 29, Last annotation update)
in similar to vertebrate nuclear recep
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; Craniata; Vertebrata; Eu
Teleostei; Ostariophysi;
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PNUCLEOTIDE SEQUENCE.

Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Na Anthoused S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

Craud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

Kallis M., Volff JN., Guigo R., Zowy M.C., Mesirov J.,

Antindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi P.,

Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
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Best Loc
Matches
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13-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                     Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygli; Neopterygli; Teleostei;
Acanthomorpha; Acanthopterygli; Percomoz
Tetradontoidea; Tetraodontidae; Tetraodo
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(TrEMBLrel. 31, Last sequence update)
(TrEMBLrel. 31, Last annotation update)
6 SCAF14768, whole genome shotgun sequ
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58.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                        raniata; Vertebrata; Euteleostom
Leostei; Euteleostei; Neoteleost
Percomorpha; Tetraodontiformes;
Tetraodon.
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RESULT 14
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NUCLEOTIDE
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ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; STKC; 1.

SMART; SM00211; TyrkC; 1.

SMART; SM00211; PROTEIN_KINASE_DOM;
NOW TEE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mature oocytes (By similarity).
EMBL; CAAE01011768; CAG05517.1; -; Ge
InterPro; IPR0007719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.

FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of the Ry similarity).

SUBUNIT: Forms a stable but non-covalent complex with cyclin B in the control of the control o
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Matches 258; Conser
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EDERT L., Schick M., Neubert P., Schatten R., Submitted (JUN-2004) to the EMBL/GenBank/DDB.

EMBL; AL137662; CAB70864.1; -; mRNA.

EMBL; CR457350; CAG33631.1; -; mRNA.

PIR; T46491; T46491.

GO: GO:0005524; F:AATP binding; IEA.

GO: GO:0004672; F:protein kinase activity; IE
GO: GO:0006468; P:protein amino acid phosphor
InterPro; IPRO00719; Prot. kinase.
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PS TETNG
Q4RKP5 TETNG
Q4RKP5;
13-SEP-2005 (13-SEP-2005 (13-SEP-
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Q9NSYO;
01-OCT-2000 (
01-OCT-2000 (
01-FEB-2005 (
                                       (Fragment)
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(Fragment)
(Frammes=GSTENG00032841001;

Tetraodon nigroviridis (Green puffer).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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Hypothetical protein; Nucleotide-binding.
SEQUENCE 258 AA; 29852 MW; 3C886AAD4CDE26EA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last samotation update)
Hypothetical protein DKFZp434P086 (LOC340371 protein)
Name=DKFZp434P086; Synonyms=LOC340371;
                                                                                                                                                                                                                                                                                                                                             Chromosome 5
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Submitted (JAN-2000)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Testis;
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    Created)
    Last sequence update)
    Last annotation update)
    whole genome shotgun sequen

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EMBL/GenBank/DDBJ
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Pred. No. 4.4e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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rimates; Catarrhini; Hominidae;
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RP NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Nicaud C., Salanoubat M., Levy M., Boudet N., Castellano S.,

RA Anthousard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Duprat S., Hortier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Duprat S., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Cruaud G., Larder G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Wincker P., Lander B.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

RT the early vertebrate proto-karyotype.";

RA Nature 431:946-957 (2004).
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Best Local 9
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SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
NON_TER 1 1 1
NON_TER 483 A83
SEQUENCE 483 AA; 54608 MW; 1A970E4D3
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                                          HGNLTSDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                     NFKQLEEKVKAVFDNLIHLEHANIVKFHKYWADTKDGRARVIFITEYMSSGSLKQFLKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKT 138
AELPRPRRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQ 411
                                                                                                                                         EYGDDNVTTAVDÍYSFGMCVLEMÁLLEÍHGNGESSYVSQDAÍNNAIQLLEDFLQKELÍQK 293
                                                                                                                                                                        EYGEVADGTAVDIFSFGMCALEMAVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILC 291
                                                                                                                                                                                                                                                                                                                                        KKNHKTMNEKALKRWCTQILSALKTLTSVQALGQDAVKSSLLMFSFPICSYLHSSDPPII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.9%; Score 1331.5; DB 2; Length 483; 53.6%; Pred. No. 1.1e-87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 114;
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Search completed: January 12, Job time : 78 secs 2006, 11:21:58

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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    GenCore version 5.1.6 (c) 1993 - 2006 Compugen
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                      US-10-618-941-99
US-10-840-512-185
US-09-840-787-20
US-10-989-228-10
US-10-989-228-10
US-10-989-228-10
US-10-153-668-329
US-10-040-647-10
US-09-764-875-799
US-10-997-143-2798-1714
US-11-997-143-2798-1714
US-10-040-848-822
US-09-764-875-1053
US-09-764-875-1053
US-09-764-875-1053
US-09-764-875-750
US-09-764-875-750
US-09-862-027-36
US-09-862-027-35
US-10-989-228-35
US-10-989-228-35
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US-10-433-794-17
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Sequence 99, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 20, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 609, App
Sequence 609, App
Sequence 270, App
Sequence 270, App
Sequence 1714, Ap
Sequence 1714, Ap
Sequence 2068, App
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
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Sequence 108, Appl
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US-10-618-941-99
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359.5	359.5	363.5	365.5	365.5	367.5	367.5	368.5	368.5	370.5	370.5	371.5	372	372	376.5	378	378	386
13.5	13.5	13.6			13.8	13.8	13.8	13.8	13.9	13.9	13.9	13.9	13.9	14.1	٠	٠	14.5
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US-10-491-467-2	US-10-052-648A-38	US-10-437-963-103929	US-10-425-114-72414	US-10-424-599-170860	US-10-114-270-80	US-10-052-648A-12	US-10-989-228-40	US-09-862-027-40	US-10-196-935A-4	US-10-052-648A-37	US-10-478-146-8	US-10-989-228-34	US-09-862-027-34	US-10-052-648A-36	US-10-460-545-2	US-10-182-243-50	US-10-840-512-197
Sequence 2, Appli	Sequence 38, Appl	Sequence 103929,	Sequence 72414, A	Sequence 170860,	•	•	•	40	Sequence 4, Appli	Sequence 37, Appl	Sequence 8, Appli	Sequence 34, Appl	•	Sequence 36, Appl	Sequence 2, Appli	Sequence 50, Appl	Sequence 197, App

## ALIGNMENTS

```
Sequence 99, Application US/10618941
Publication No. US20040197792A1
GENERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SERAE
APPLICANT: CAENEPEEL, SIANASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR APPLICATION NUMBER: 50/395,632
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PATENTIA VERSION 3.2
SEQ ID NO 99
LENGTH: 507
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                              US-10-618-941-99
Query Match
Best Local Similarity
Matches 507; Conservat
  Conservative
                              100.0%; Score 2670; DB 4; 100.0%; Pred. No. 1.4e-220
  0,
     Mismatches
                              1.4e-220;
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  Indels
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507;

Matches	507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Ϋ́	1 MAAPEPAPRRAREREREDESEDESDILEESPCGRWQKRREQVNQGNWPGLQSTFLAMD 60	
9	1 MAAPEPAPRRAREREREREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMD 60	
Ş	61 TEEGVEVVWNELHFGDRKAFAAHEKKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVI 120	
9	61 TEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVI 120	
Ϋ́	121 FITEYVSSGSLKQFLKKTKKNHKAMNARAWKFWCTQILSALSFLHACSPPIIHGNLTSDT 180	
9	121 FITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDT 180	
ΥÇ	181 IFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADG 240	
8	181 IFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADG 240	
Ş	241 TAVDIFSFGMCALEMAVLEIQTNGDTRVTEEAIARARHSLSDPNMREFILCCLARDPARR 300	
9	241 TAVDIFSFGMCALEMAVLEIQTNGDTRVTEEAIARARHSLSDPNMREFILCCLARDPARR 300	
Ϋ́	301 PSAHSLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRP 360	
ъ	301 PSAHSLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELFRPRRP 360	

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APPLICANT: CHARYDCZAK, GLEN
APPLICANT: GRIGORIEV, ICOR
ITITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-1455
CURRENT APPLICATION NUMBER: US/10/840,512
CURRENT FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: 60/469,014
PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 239
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 185
LENGTH: 499
TYPE: PRT
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US-10-840-512-185
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Best Local S
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                                                       PDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHY
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     GFLHEDDRMKLAAFLESTFLKYRGTQA 507
                                                                                                                          PLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEP
                                                                                                                                                                                                PSAHSILFHRVLFEVHSIKKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRP
                                                                                                                                                                                                                                                                                                                   IFIQHNGLIKIGSVWYRIFSN-----ALPDDLRSPIRAEREELRNLHFFPPEYGEVNDG
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                                                                                                        PMQWRYSEVSFLELDKFLEDVRNGIYPLMNFAAARPLGLPRVLAPPPEEAQKAKTPTPEP
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93.9%; Pred. No. 6.8e-206;
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US-09-862-027-10
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                                                                                                  Sequence 10, Application US/10989228
Publication No. US20050089917A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: Novel Kinases and Use:
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/10/989,228
CURRENT FILING DATE: 2004-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATENT NO. US20020142428A1

GENERAL INFORMATION:

APPLICANT: Hodge, Martin R.

TITLE OF INVENTION: NO. US20020142428A1el Kinases and Uses Thereof

FILE REFERENCE: 35800/234862

CURRENT PILLYS ONTE: 2001-05-21

PRIOR APPLICATION NUMBER: US 09/345,473

PRIOR FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10
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Best Local Similarity
Matches 301; Conserv
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PRIOR APPLICATION NUMBER: US/09/862,027
PRIOR FILING DATE: 2001-05-21
PRIOR PPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FABESEQ for Windows Version 4.
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TYPE: PRT
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FEATURE:
NAME/KEY: VARIANT
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OTHER INFORMATION: Xaa =
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Pred. No. 4e-127;
0; Mismatches 2;
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US-09-840-787-20
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; LOCATION: (1)...(326)
; OTHER INFORMATION: Xaa =
US-10-989-228-10
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09840787
Patent No. US20020058264A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
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Best Local Similarity
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                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FABELSEQ for Windows Version 2.

CURRENT APPLICATION NUMBER: US/09/840,787

FILING DATE: 23-Apr-2001

CLASSIFICATION: <Unknown>
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ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            Guegler, Karl J.
Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
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                                                                                                                                                                                                  CITY: Palo Alto
STATE: CA
COUNTRY: USA
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   APPLICATION NUMBER: 09/518,865 FILING DATE: <Unknown>
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Bandman, Olga
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97.4%;
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           Sequence 322, Application US/10153668
Publication No. US20030092616A1
GENERAL INFORMATION:
APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATSU, Shuji
APPLICANT: SHIZAMA, Kenya
ITILB OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1354-0207P
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US-10-153-668-322
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Best Local 9
CURRENT APPLICATION NUMBER: US/10/153,668
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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Similarity 61.6%;
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315 VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFME
                       428 VIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFLHEDD
                                                                                                                                                                            330 VPSLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQTLYSQSPALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK
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VVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEAD
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Pred. No. 6.5e-123;
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CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR PILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: JP 2001-313175
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US-09-764-875-749
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                                                   Sequence 749, Application US/09764875
Publication No. US20040018969A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PJZ02
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Best Local S
Matches 305
                   CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Prior application data removed -
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61.6%;
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                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10059585
Publication No. US20030082776A1
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 749
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Best Local (
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                            Nishikawa,
                                                                                                                                                                                                                                                        Hayashi, Koji
Otsuka, Kaoru
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APPLICANT: Yamamoto, Jun-ichi
APPLICANT: Ishii, Shizuko
APPLICANT: Sugiyama, Tomoyasu
APPLICANT: Wakamatsu, Ai
APPLICANT: Wakamatsu, Ai
APPLICANT: Nagai, Keiichi
APPLICANT: Otsuki, Tetsuji
APPLICANT: Funahashi, Shin-Ichi
APPLICANT: Senoo, Chiaki
APPLICANT: Nezu, Jun-Ichi
APPLICANT: NOWEL GENES ENCODING PROTEIN
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-09803
CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2002-01-29
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Pred. No. 7.26
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7.2e-123;
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RESULT 9
US-10-040-647-10
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; ORGANISM: Homo sapiens
US-10-059-585-2
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PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR PELICATION NUMBER: JP 2000-118776
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 11-248036
PRIOR PILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                               Sequence 10, Application US/10040647
Publication No. US20030092154A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 535
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APPLICANT: (US only) ANTALIS Toni Marie in TITLE OF INVENTION: NOVEL MOLECULES NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESSE: SCULLY, SCOTT, MURPHY & STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY
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APPLICATION NUMBER: US 60/183,322
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Similarity 61.4%;
04; Conservative 5:
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Pred. No. 1.7e-122;
99; Mismatches 103; Indels 29;
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Matches 301; Conservat
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TELEPAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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FILING DATE: Chrhown
APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
APPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
APPLICATION NUMBER: INTERNATION:
APPLICATION NUMBER: PO5101/97
APPLICATION N
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
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APPLICATION NUMBER: US/10/040,647
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
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VVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEAD
                                         VIOMOCNIERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFLHEDD
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REGISTRATION NUMBER: 31,346
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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US-09-925-297-609
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Best Local S
Matches 293
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NUMBER OF SEQ ID NOS: 928
SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 609
LENGTH: 501
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CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR TILING DATE: 10/124,270
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TITLE OF INVENTION: Nucleic
FILE REFERENCE: PA105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa equals
NAME/KEY: SITE
LOCATION: (30)
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NAME/KEY: SITE
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ORGANISM: Homo sapiens
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                    477
                                                      399
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                                                                                                                                                                                                                                                                                                                                                                 186 NGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREBLRNLHFFPPPEYGEVAD-GTAVD
                                                                                                                                                                                                                                                                                                                                                                                                               119 MSSGSLKQFLKKTKKNHKINNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQH
                                                                                                                                                                                                                                304 HSLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                        126 VSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQH 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
LVHYGFLHEDDRMKLAAFLESTFLKY
                                                                     TPEPFDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASE 476
                                                                                                                                                                                                                                                                                        IFSFGMCALEMAVLEIQTNGDTR-VTEBAIARARHSLSDPNMRBFILCCLARDPARRPSA
                                                  TPEPAEVETRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAE
                                                                                                                             QTLYSQSPALELDKFLEDVRNGIYPLTAF----
                                                                                                                                               QWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEV-----QKAKTP
                                                                                                                                                                                                RELLFHPALFEVPSLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPV
                                                                                                                                                                                                                                                                                                                                              NGLIKIGSV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POPOLLPORKKKKVKMS----LRFWKSRPVGXXQKRREEVNORNVPGIDSAYLAMDTEEGV
                                                                                                                                                                                                                                                                     IYSFGMCALEMAVLEIQGNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.1%; Score 1444; DB 3;
57.9%; Pred. No. 3.6e-115;
Live 64; Mismatches 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       naturally occurring
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RESULT 12 US-11-097-143-270

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314 269 255 221 196

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Sequence 270, Application US/11097143 Publication No. US20050208558A1

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PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR RPLICATION NUMBER: US 60/328,403
PRIOR RPLICATION NUMBER: US 60/328,403
PRIOR APPLICATION NUMBER: UP 2001-157043
PRIOR APPLICATION NUMBER: UP 2001-260681
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: UP 2001-313175
PRIOR PILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
SOFTWARE: PATENTIN OF SEQ ID NOS: 488
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US-10-153-668-434
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Publication No. US20030092816A1
GENERAL INFORMATION:
APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
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Best Local Similarity
Matches 263; Conserv
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CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STATE Activating Gene
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                                                374
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390
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                                                                                                                                   VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFME
                                                                                                                                                                                                                                      AVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE
                                                LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPFDSET 425
                                                                                                                                                                                                                                                                                                           ------APDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEM
                                                                                                                                                                                                                                                                                                                                         RIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVAD-GTAVDIFSFGMCALEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKAFAAHBEKIQTVEBQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEEEESEDESEILEESPCGRWQKRREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSE
  LDKFLEDVRNGIYPLTAF----
                                                                                                                                                                                                      AVLEIQGNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFE
                                                                                                                                                                                                                                                                                                                                                                                                            KTKKNHKTMNEKAWKRWCTOILSALSYLHSCOPPIIHGNLTCDTIFIQHNGLIKIGSV--
                                                                                                                                                                                                                                                                                                                                                                                                                                            KTKKNHKAMNARAWKRWCTQILSALSFLHACSPFIIHGNLTSDTIFIQHNGLIKIGSVWH
                                                                                                     VPSLKLLAAHCIVGHOHMIPENALEEITKNMDTSAVLAEIPAGPGREPVOTLYSOSPALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
-GLPRPQQPQQEEVTSPVVP-PLCQDSDT
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FILLE OF INVESTATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PRIOR DATE: 1999-10-28
PRIOR PRIOR DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-3,383
PRIOR FILING DATE: 1999-11-3,383
PRIOR FILING DATE: 1999-12-8
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-03-3
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 270
LENGTH: 637
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; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-270
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Best Local Similarity
Matches 245; Conserv
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: ARRAYS, FOR DETECTING
TITLE OF INVENTION: DROSOPHILA GENES.
549
                              482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLFEVHSLKILAAHCFIQHQYIMPENVVEEKTKAMD-----LHAVLAELPRPRRPPI
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                            FLHEDDRMKLAAFLEST 498
                                                                                             DSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYG
                                                                                                                                                       OWRYSEVSFME-LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPF
                                                                                                                                                                                                  LLFEVHSLKILTAHCLV----FSPANRTMFSETAFDGLMQRYYQPDVVMAQLRLAGGQER
                                                                                                                                                                                                                                                                                                                                            -----VPDAVHYSVRRGRERERERERGAHYFQAPEYGAADQLTAALDIYAFGMCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEA-CARVIFITEYVSSGSLKQF
                                                                                                                                 QYRLADVSGADKLEKFVEDVKYGVYPLITYSGKKPPNF-RSRAASPERADSVKSATPEPV
                                                                                                                                                                                                                                                                       LEMAALBIOPSNSESTAINEETIORTIFSLENDLORDLIRKCLNPOPODRPSANDLIFHP
                                                                                                                                                                                                                                                                                                LEMAVLEIQTNG--DTRVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHR 310
                                                               DTESRRIVNMMCSVKIKEDSNDITMTILLRMDDKMNRQLTCQVNENDTAADLTSELVRLG
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Pred. No. 7.4e-92;
7; Mismatches 146;
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EXPRESSION OF
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NAME/KEY: SITE
LOCATION: (307)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (319)
OTHER INFORMATION: X
US-09-764-868-798
RESULT 14
US-09-764-875-1053
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SEQ ID NO 798
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic A
FILE REFERENCE: PTZ32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-764-868-798
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to
NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (274)
OTHER INFORMATION:
NAME/KEY: SITE
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NAME/KEY: SITE
LOCATION: (296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                              117 ARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPFIHGNL
                                                              285
                                                                                                                                                                                                       295 RDPARRPSAHSLIFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAEL
                                                                                                                                                                                                                                            111
                                                                                                                                                                                                                                                         237 VAD-GTAVDIFSFGMCALEMAVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLA
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                                                             VVP-PXVKDFHTXTSLRWRL-----
                                                                                         KTPTPEPFDSETRKVIOMQCNLERSEDKARWHL 446
                                                                                                                                              PR-PRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKA
                                                                                                                                                                                 SEPARRPTARELLFHPALFEVPSLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEI
                                                                                                                                                                                                                                         VTNVTTAVDIYSFGMCALEMAVLEIQGNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQ
                                                                                                                                                                                                                                                                                                     TCDTIFIQHNGLIKIGSV------APDTINNHVKTCREEQKNLHFFAPEYGE
                                                                                                                     PAGPGREPVQTLYSQSPALELDKFLEDVRNGIYPLTAF----
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                                                                                                                                                                                                                                                                                                                                                                                                                         35.4%; Score 946; DB 3; 60.4%; Pred. No. 1.4e-72; cive 29; Mismatches 71
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Sequence 1053, Application US/09764875
Publication No. US20040018969A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Pr

Proteins,

and

Antibodies

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US-10-292-798-1714
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1053
TENGTH: 340
                                                                                                                                                                                                                                           Sequence 1714, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: UF 2001-246789
PRIOR FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.4%; So
Best Local Similarity 60.4%; Pr
Matches 201; Conservative 29;
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NAME/KEY: SITE
LOCATION: (296)
OTHER INFORMATION: )
NAME/KEY: SITE
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (307)
OTHER INFORMATION: Xaa equals any of the naturally occurring NAME/KEY: SITE
LOCATION: (319)
OTHER INFORMATION: Xaa equals any of the naturally occurring
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 VAD-GTAVDIFSFGMCALEMAVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARVIFITEYMSSGSLKQFLKKTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNL
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Pred. No. 1.4e-72;
9; Mismatches 71;
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; ORGANISM: Homo
US-10-292-798-1714
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Best Local Similarity 42.2%; Pred. No. 1.2e-66;
Matches 201; Conservative 39; Mismatches 67
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1714
LENGTH: 752
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LMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISE
                              QMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLFTDSAQDLASELVHYGFLHE
                                                                                       KFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPPEEV-----QKAKTPTPEPFDSETRKVI
                                                                                                                                                     SLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLABLPR-PRRPPLQWRYSEVSFMELD
                                                                                                                                                                                                                      VLEIQTNGDTRVTEBAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFEVH
                                                                                                                                  SLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQ------
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                                                                 -GLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRKVV
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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199
1992
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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       GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd.
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 US-10-821-234-1137
US-10-661-426-7
US-11-134-563-16
US-10-661-426-42
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US-10-70-726-71
US-10-70-726-83
US-10-770-726-83
US-10-770-726-85
US-11-09-156-12
US-11-09-156-12
US-11-09-156-14
US-11-113-424-183
US-11-004-057-6
US-11-004-057-6
US-11-004-057-4
US-11-004-057-4
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US-11-103-065-4
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Sequence 1137, Ap
Sequence 7, Appli
Sequence 16, Appli
Sequence 13, Appl
Sequence 131, Appl
Sequence 131, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 21, Appl
Sequence 308, Appl
Sequence 41, Appl
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US-10-821-234-1137

Sequence 1137, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT APPLICATION NUMBER: US 60/462,047

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt SEQ_genes Version 1.0

LENGTH: 588

TYPE: PRT

ORGANISM: Homo sapiens
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## ALIGNMENTS

of.

Preeclampsia

Qy 251 CALEMAVLEIQTNGDTRVTEEAIARARHSLSDPNMREFI 289	Db 230 AFLATGGDITRNKVRKTFVGTPCWMAPEVMEQVRGYDFKADIWSFGI 276	Qy 198 IFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADGTAVDIFSFGM 250	Db 172 GEHKSGVLDESTIATILREVLEGLEYLHKNGQIHRDVKAGNILLGEDGSVQIADFGVS 229	Qy 140 KNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHR 197	Db 116 TSMDELLKEIQAMSQCHHPNIVSYYTSFVVKDELMLVMKLLSGGSVLDIIKHIVAK 171	Qy 89 TVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTK 139	Db 69 LPWSINRDDYELQEVIGSGATAVVQAAYCAPKKEKVAIKRINLEKCQ 115	Qy 35 GRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQ	Db DPAPRRPTRGCSETIGGGAAAAAAAVGGGETRGEETSEVSEFEGGPRAAAAVMSEDSSA 68	Qy 5 EPAPRR	Query Match 7.5%; Score 199; DB 6; Length 588; Best Local Similarity 20.6%; Pred. No. 7e-10; Matches 125; Conservative 87; Mismatches 213; Indels 1
EAIARARHSLSDPNMREFI 289	TPCWMAPEVMEQVRGYDFKADIWSFGI 276	FFPPEYGEVADGTAVDIFSFGM 250	IHRDVKAGNILLGEDGSVQIADFGVS 229	PIIHGNLTSDTIFIQHNGLIKIGSVWHR 197	3LWLVMKLLSGGSVLDIIKHIVAK 171	ACARVIFITEYVSSGSLKQFLKKTK 139	CEKVAIKRINLEKCO 115	CEEGVEVVWNELHFGDRKAFAAHEEKIQ 88	RGEETSEVSEFEGGPRAAAAVMSEDSSA 68	REREREDESEDESDILEESPC 34	DB 6; Length 588; -10; 3 213; Indels 182; Gaps 27;

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US-10-661-426-7
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SEQ ID NO 7
LENGTH: 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.2%; Score 192; DB 6; Best Local Similarity 22.6%; Pred. No. 1.5e-09; Matches 82; Conservative 53; Mismatches 122
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CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
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NUMBER OF SEQ ID NOS: 16
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APPLICANT: Ausubel, Trederick M.
APPLICANT: Asai, Teuneaki
APPLICANT: Tena, Guillaume
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                                                                                                                                                                                                                                                              111 YGNHEETVRRQICREIEILRDVNHPNVVKCHEMFDQNGE----IQVLLEFMDKGSLE---
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277 TAIELATGAAPYHKYPPMKVLMLTLQNDPPSLETGV-----QDKEMLKKYGKSFRKMI
                                                                                                                                                                                                               136 KKTKKNHKAMNARAWKR-----WCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIK 190
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                                                                                                                                                                                                                                                                                                      ---HEEKIQ----TVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFL 135
                                                                                                                                                                                                                                                                                                                                             SGSAPSSGGSASSTNTNSSIEAKNYSDLVRGNRIGSGAGGTVYKVIHRPSSRLYALKVI
    GDIWSLGVSILEFYLGRFPFPVSRQGDWASLMCAICMSQPPEAPATASPEFRHFISCCLQ
                                            VDIFSFGMCALEMAV----LEIQTNGDTRVTEEAIARAR----HSLSDPNMREFILCCLA
                                                                                                                                                                        -----GAHVWKEQQLADLSRQILSGLAYLH--SRHIVHRDIKPSNLLINSAKNVK
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                                                                                        IADFGVSRILAQDMDPC-----
                                                                                                                                IGSVW-HRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPE-----YGEVADGTA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Mismatches 122;
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US-11-134-563-16

Sequence 16, Application US/11134563

Publication No. US20050287569A1

GENERAL INFORMATION:

APPLICANT: Leong, John M.

APPLICANT: Campellone, Kenneth G.

TITLE OF INVENTION: ESEPTU NUCLEIC ACIDS AND PROTEINS AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 07917-280001

CURRENT APPLICATION NUMBER: US/11/134,563

CURRENT APPLICATION NUMBER: US 60/573,600

PRIOR APPLICATION NUMBER: US 60/573,600

PRIOR APPLICATION STATE: 2004-05-20
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US-10-661-426-4
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; ORGANISM: Homo
US-11-134-563-16
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publication No. US20050262584A1
GENERAL INFORMATION:
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SOFTWARE: FRANCEQ for Windows
SEQ ID NO 16
LENGTH: 545
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APPLICANT: Sheen, Jen
APPLICANT: Ausubel, Frederick M.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Tena, Guillaume
TITLE OF INVENTION: Master Activators of Pathogen Responsive
FILE REFERENCE: 00786/397003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPII 172
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Pred. No. 3.2e-09;
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Gaps

284

333

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230

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386

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GENERAL INFOGRATION:

APPLICANT: Sheen, Jen
APPLICANT: Ausubel, Frederick M.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Tena, Guillaume
ITILE OF INVENTION: Master Activators of Pathogen Responsive
ITILE OF INVENTION: Genes
FILE REFERENCE: 00786/397003
CURRENT APPLICATION NUMBER: US/10/661,426
CURRENT FILING DATE: 2003-09-12
FRIOR FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
INUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
LEUGTH: 366
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-661-426-13
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US-10-661-426-13
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; TYPE: PRT
; ORGANIZM: Arabidopsis thaliana
US-10-661-426-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/10661426 Publication No. US20050262584A1 GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 16
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22.3%; Pred. No. 2.2e-09;
ative 54; Mismatches 122;
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US-10-878-556A-131
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SEQ ID NO 131
LENGTH: 524
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw hum/pak2_human
DATABASE ENTRY DATE: 1997-11-01
                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 131, Application US/10878556A
Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: Hoffmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762
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                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
                                                                                                                                                                                                                                                                                                                                       Local Similarity
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361 A--NQVIHRDIKSDNVLLGMEGSVKLTDFG---FCAQI-----TPEQSKRSTMV
                                       166 ACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELR
                                                                                                           106 HKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLH
                                                                                                                                                          259 --ASGTVFTATDVALGQEVAIKQINL-----QKQPKKELIINEILVMKELKNPNIVN-
                                                                                                                                                                                                                                      201 PVPAPVGDSHVDGAAKSLDKOKKKPKMTDEEIMEKLRTIVSIGDPKKKY-TRYEKIGOG-
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                                                                                                                                                                                                                                                                                                                       80;
                                                                                                                                                                                                                                                                            4 PEPAP-----RRAREREREREDESEDESDILEE-----SPCGRWQKRREQVNQGN
                                                                            ---FLDSYLVGDELFVVMEYLAGGSLTDVVTET----CMDEAQIAAVCRECLQALEFLH
                                                                                                                                                                                               MPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVL---VDHPNIVKL 105
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                                                                                                                                                                                                                                                                                                                 6.9%; Score 184.5; DB 6;
23.3%; Pred. No. 1.1e-08;
ative 60; Mismatches 126;
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US-10-661-426-12
; Sequence 12, Application US/10661426
; Publication No. US20050262584A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Asai, Tsuneaki
; APPLICANT: Tena, Guillaume
; TITLE OF INVENTION: Master Activators of Pathogen Res
; TITLE OF INVENTION: Genes
; FILE REFERENCE: 00786/397003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liu, wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AMIO1079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                    RESULT 8
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US-10-770-726-71
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Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 72; Conserv
     CURRENT APPLICATION NUMBER: US/10/661,426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 GNLTSDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFF--P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 EACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 GSTGIVCIATVRSSGKLVAVKKMDLRKQQRRELLFNEVVIMRDYQHENVVEMYNSYLVGD
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                                                                                                                                                                                                                                                                                                                                                                            539 HKVSPSLKGFLDRLLVRDPAQRATAAELLKHPFL 572
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US-10-523-477-11
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                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-10-523-477-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 12
LENGTH: 348
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/10523477 Publication No. US20050266406A1 GENERAL INFORMATION:
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Best Local Similarity
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PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MAXS AS MODIFIERS OF THE AXIN PATHWAY AND METHODS OF FILE REFERENCE: EX03-051C-US CURRENT PEPLICATION NUMBER: US/10/523,477
CURRENT FILING DATE: 2005-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/401,534
PRIOR FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/411,153
PRIOR FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: EXELIXIS,
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 403
                                                                                                                                                                                                                                                                        Match 6.3%;
Local Similarity 24.0%;
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                                                                                                                                                  104 SAPENNP----EEELASKQKNEESKKRQWALEDFEIGR----PLGKGK---FGNVYLA 150
119 VIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTS 178
                                                151 REKQSKFILALKVL-FKAQLEKAGVEHQLRREVEIQSHLRHPNILRLYGYFHDAT----R
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                                                                                                 59 MDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACAR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 VYKVIHTPTSRPFALKVIYGNHEDTVRRQICREIEILRSVDHPNVVKCH----DMFDHNG 139
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                                                                                                                                                                                                2 AAPEPAPRRARERE---REREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLA 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APATASQEFRHFVSCCLQSDPPKRWSAQQLLQH
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                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              version 3.2
                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                           Score 168.5; DB 6; Pred. No. 2e-07;
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                 131;
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FILE REFERENCE: AM101079 (031896-01000);
CURRENT APPLICATION NUMBER: US/10/770,726;
CURRENT FILING DATE: 2004-02-04;
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2;
SEQ ID NO 83;
LENGTH: 403;
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-770-726-83
          RESULT 11
US-10-770-726-85
; Sequence 85, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
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US-10-770-726-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCERS
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wyeth
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                                                                                                                                               LKHNPSORPMLREVLEH 380
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                                                                                                                                                                                                                                                                                                                                             VYLILEYAPLGTVYRELQKLSKFDEQRTA----TYITELANALSYCH--SKRVIHRDIKP
                                                                                                                                                                                                                                                                                                                                                                           VIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTS 178
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                                                                                                                                                                                                             MHD-EKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLISRL
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Brown, Eugene
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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          CURRENT APPLICATION NUMBER: US/11/109,156
CURRENT FILING DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/10/060,065
PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05061
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR APPLICATION NUMBER: US 60/159,590
                                                                                                                         APPLICANT: Jun-Ichi Nezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION: PHOSPHATASE
FILE REFERENCE: 06501-099002
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                          Keiichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
                                                                                                                                                                                              Chiaki Senoo
                                                                                                                                                                                                                                                                                          Jun-Ichi Yamamoto
Shizuko Ishii
                                                                                                                                                                                                                                                                                                                                          Koji Hayashi
                                                                                                                                                                                                                                                                                                                                                           Tetsuo Nishikawa
                                                                                                                                                                                                                                                                                                                                                                           Takao Isogai
                                                                                                                                                                                                                                                                           Tomoyasu Sugiyama
                                                                                                                                                                                                                                                             Wakamatsu
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KINASE/PROTEIN

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; ORGANISM: Homo sapiens
US-10-770-726-85
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SEQ ID NO 85
LENGTH: 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
FULL REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATE 2004-02-04
NUMBER OF SEQ ID NOS: 48640
                                               293 LARDPARRPSAHSLLFH 309
                                                                                                                                           237 VADGTAVDIFSFGMCALEMAVLEIQTNGDT-RVTEEAIARARHSLSD---PNMREFILCC
                                                                                                                                                                                                                                                                                                                                                                                                       151 REKQSKFILALKVL-FKAQLEKAGVEHQLRREVEIQSHLRHPNILRLYGYFHDAT----R
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LKHNPSQRPMLREVLEH 380
                                                                                                   MHD-EKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLISRL
                                                                                                                                                                                                  ENLLLGSAGELKIAD-----FGWSVHAPSSRRTTL-
                                                                                                                                                                                                                                                 DTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEY--GE 236
                                                                                                                                                                                                                                                                                                      VYLILEYAPLGTVYRELQKLSKFDEQRTA----TYITELANALSYCH--SKRVIHRDIKP
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US-11-092-168-1
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US-11-109-156-12
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Best Local :
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SEQ ID NO 12
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APPLICANT:
APPLICANT:
                                                       APPLICANT: Della Croce, Kimiko
APPLICANT: Von Hoff, Daniel D.
APPLICANT: Grand, Cory L.
TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
FILE REFERENCE: 920214.00003CONT3
CURRENT APPLICATION NUMBER: US/11/092,168
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: US 10/965,313
                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICANT: Hurley, Laurence H.
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PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR PPLICATION NUMBER: JP 2000-241899
PRIOR PILING DATE: 2000-06-09
UNMBER OF SEO ID NOS: 43
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$ 60/608,529
$ 60/511,486
$ 60/511,489
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Similarity 24.0%;
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Vankayalapati, Hariprasad
Bashyam, Sridevi
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Hurley, Laurence H.
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Pred. No. 2e-07;
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US-10-661-426-9
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                                                                                                                         ; ORGANISM: Arabidopsis thaliana
US-10-661-426-9
                                                                                                                                                            SEQ ID NO 9
LENGTH: 348
TYPE: PRT
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1
LENGTH: 403
TYPE: PRT
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Best Local Similarity
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Master Activators of Pathogen Responsive TITLE OF INVENTION: Genes FILE REFERENCE: 00786/397003
CURRENT APPLICATION NUMBER: US/10/661,426
CURRENT FILING DATE: 2003-09-12
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2004-09-09
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                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/275,199 PRIOR FILING DATE: 2001-03-12
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                                                                      Local
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68 VMNELHFGDRKAFAA-----HEEKIQ----TVFEQLVLVDHPNIVKLHKYWLDTSEACA 117
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                                                                   6.3%;
Similarity 24.2%;
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Tena, Guillaume
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Pred. No. 2e-
                                                                      Score 167.5;
Pred. No. 2e-
                                                      Mismatches
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RESULT 15

US-10-661-426-14

; Sequence 14, Application US/10661426

; Publication No. US20050262584A1

; GENERAL INFORMATION:
Search completed: January 12, 2006, 11:33:39 Job time : 32 secs
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SOFTWARE: FABCSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-661-426-14
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CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Master Activators of Pathogen Responsive TITLE OF INVENTION: Genes
                                                                                                                                                                           231 PERINTDLNHGRY-DGYAGDVWSLGVSILEFYLGRFPFAVSRQGDWASLMCAICMSQPPE 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 VWNELHFGDRKAFAA-----HEEKIQ----TVFEQLVLVDHPNIVKLHKYWLDTSEACA 117
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Asai, Tsuneaki
Tena, Guillaume
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-Qe/cgn2 1/USPTO_spool_p/US10618941/runat_12012006_070207_14416/app_query.fasta_1.647
-Qe/cgn2 1/USPTO_spool_p/US10618941/runat_12012006_070207_14416/app_query.fasta_1.647
-Qe/cgn2 1/USPTO_spool_p/US10618941/runat_12012006_070207_14416/app_query.fasta_1.647
-DB=PublIshed_ApplicatIons Na_New -QFNT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=blts -STRAT=1 -END=-1 -MATRI-blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -HRAPSIZE=500 -MINLEN=0
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HRAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US10618941 @CGN 1 1 184 @Tunat 12012006_070207_14416
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Maximum DB seq length: 200000000
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US-10-955-054A-44

US-11-136-527-688

US-10-770-726-27

US-10-821-234-285

US-10-661-426-6
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US-11-128-061-2970
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## ALIGNMENTS

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Hann, Louane E.

JCANT: Sinacore, Markin S.

APPLICANT: Leonard, Mark W.

APPLICANT: Brown, Eugene L.

APPLICANT: Miller, Christopher P.

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS

TITLE OF INVENTION: TO MONITOR GENE EXPRESSION

FILE REFERENCE: 01997.027701

CURRENT APPLICATION NUMBER: US/11/128,061

CURRENT APPLICATION NUMBER: US/11/128,061

PRIOR APPLICATION NUMBER: US/11/128,061

PRIOR FILING DATE: 2005-05-11

NUMBER OF SEQ ID NOS: 7285

SOFTWARE: Patentin version 3.3

SEQ ID NO 2970

IENGTH: 540

TYPE: DN"
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 Percent Similarity:
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NUMBER OF SEQ ID NOS: 7285
SOSTWARE: PatentIn version 3.3
SEQ ID NO 6612
LENGTH: 540
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Hann, Louane Martin S.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6612, Application US/11128061 Publication No. US20060003958A1
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APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miler, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO TITLE OF INVENTION: TO MONITOR GENE EXPRESSION FILE REFERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
                                                                                                                                                                   Local Similarity:
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                                                   GluArgGluAspGluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArg
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 TrpGlnLysArgArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPhe
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APPLICANT: Wang, Tongtong
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 669
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 642, 661
COTHER INFORMATION: n = A,T,C or G
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; Sequence 23, Application US/10623155
; Publication No. US20050261166A1
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                GAGGAGGTGACATCACCTGTCGTGCCCCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCT
CAGTCACCAGCTCTGGAATTAGATAAATTCCTTGAAGATGTCAGGAATGGGATCTATCCT
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APPLICANT: SYMMANS, W. FRASER
APPLICANT: SYMMANS, W. FRASER
APPLICANT: HESS, KENNETH R.
APPLICANT: AYERS, MARK
APPLICANT: AYERS, MARK
APPLICANT: STEC, JAMES
TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHER
FILE REFERENCE: UTXC:880US
CURRENT APPLICATION NUMBER: US/10/955,054A
CURRENT FILING DATE: 2004-09-30
INUMBER OF SEQ ID NOS: 195
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 44
LENGTH: 6812
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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US-10-955-054A-44
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                  GluAlaCysAlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGln 133
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AAAGGAAAGAAGTGCATTGTTTGGTGACTGAACTTATGACGTCTGGAACACTTAAAACG
                                                                   TTAAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCCTGGGAATCCACAGTA
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                                                                                                    LeuValLeuValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSer 113
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                                                                                                                                                                                 AspSerGluThrArgLysValIleGlnMetGlnCysAsnLeuGluArgSerGluAspLys
                                                                                                                                                                                                                                                                                                                                                                                                         TrpArgTyrSerGluValSerPheMetGluLeuAspLysPheLeuGluAspValArg---
                               TyrAspLeuLeuProThrAspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGly 481
                                                                                                                                                                                                                                                                 ValLeuAlaProProGluGluValGlnLysAlaLysThrProThrProGluProPhe
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                                                                                                                       AlaArgTrpHisLeuThrLeuLeuLeuValLeuGluAspArgLeuHisArgGlnLeuThr
                                                                                                                                                        ----AAAGATAATGAAGCTATTGAGTTTTCTTTTGATTTAGAGAGA
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Mounts, William M
FILE OF INVENTION: Probe Arrays For Expression Profiling of I
CURRENT ERPERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-25
INUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 688
LENGTH: 7555
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-688
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Publication No. US20050287570A1
GENERAL INFORMATION:
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Sequence 27, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
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Best Local Similarity:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING,
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM10.1079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOPTWARE: Patentin version 3.2
SEQ ID NO 27
LENGTH: 2838
TYPE: DNA
ORGANISM: Homo sapiens
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   223
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                                                                                                                                                                                                                                                                                                                                                                                                                                     86 LysIleGlnThrValPheGluGlnLeuValLeuVal-----AspHisProAsnIle 102
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GluLeuArgAsnLeuHisPhePhe-----ProProGluTyrGlyGluValAlaAspGly
                                 GCCCAGGTGAGCAAGGAAGTGCCC
                                                                                                                                                          GTGCTCCACGCC-----CAGGGCGTCATCCACCGGGACATCCAAGAGCCGACTCGATCCTG
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                                                                                                                                                                                                                                                                                                                 ThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLysLysAsnHis 142
                                                                                                                         IleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArgIlePheSerAsnAla
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                                                          LeuArgProProThrAlaLeuProAspAspLeuArgSerProIleArgAlaGluArgGlu 222
                                                                                              CTGACCCATGATGGCAGGGTGAAGCTGTCAGAC----
                                                                                                                                                                                        PheLeuHisAlaCysSerProProIleIleHisGlyAsnLeuThrSerAspThrIlePhe 182
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      FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARB: pt SEQ genes Version 1.0
SEQ ID NO 285
LENGTH: 4529
TYPE: DNA
ORGANISM: Home sapiens
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US-10-821-234-285
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                                                                                                                                                                                                                                                                    Sequence 285, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
                                                                                                                                                                                   APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and
                                                                                                                                                                                                                                   APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
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Treatment

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1690 CCAGAGGTAGACATCTGGTCGCTGGGGATAATGGTGATTGAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ThrAlaValAspilePheSerPheGlyMetCysAlaLeuGluMetAlaValLeuGluIle 260
                                                                                                                                                                                             oLeuMetAsnPheAlaAlaThrArgProLeu---GlyLeu-ProArgValLeuAlaProP
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                                                              roProGluGluValGlnLysAlaLysThrProThrProGluProPheAspSerGluThrA
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--GGCCCTCCCCATGTTCTTCTGTCTCCA
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Qy 197 ArgilePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerPro 216  B46 TGCTTTTTTAGCAACTG-GTGGTGATATTACCCGAA	CATGAAGCTGCTAAGTGGAGTTCTGGTTCTGGATATTAT  "BABIH15LYBA1aMETABIA1AATGA1ATTPLY BOTH	69 TrpAsnGluLeuHisPheGlyAspArgLysAlaPheAlaAlaHisGluGluLysIleGln 88	Qy 11	Alignment Scores:  Pred. No.:  199.00  Score:  Percent Similarity:  131  Percent Similarity:  131  Query Match:  131  Query Matches:  211  Query Matches:  227  Query Matches:  27  Query Matches:  28  Query Matches:  29  Query Matches:  211  Query Matches:  212  Query Matches:  213  Query Matches:  214  Query Matches:  215  Query Matches:  216  Query Matches:  217  Query Matches:  218  Alignative:  38  Matches:  211  Query Matches:  211  Query Matches:  211  Query Matches:  212  Query Matches:  212  Query Matches:  213  Query Matches:  214  Query Matches:  216  Query Matches:  217  Query Matches:  218  Alignative:  38  Alignative:  38  Alignative:  38  Alignative:  38  Alignative:  38  Alignative:  38  Alignative:  30  Alignative:  31  Alignative:  31  Query Matches:  21  Query Matches:  22  Query Matches:  23  Query Matches:  24  Query Matches:  27  Query Matches:  27  Query Matches:  28  Query Matches:  29  Query Matches:  20  Query Matches:  21  Query Matches:  21  Query Matches:  21  Query Matches:  21  Query Ma
Qy 494 PheLeuGlu 496	435 LeuGluArgSerGluAspLysAlaArgTrpHisLeuThrLeuLeuValLeuGluAspLeigliaspLysAlaArgTrpHisLeuThrLeuLeuValLeuGluAspleigliaspLeigliaspLeuGluAspLeigliaspLeigliaspLeuGluAspLeigliaspLeuGluAspLeigliaspLeuGluAspLeuGlaAcCAACCAAGATCAGTCAGTACTAAGATTAAGGAATTCCAAA 455 ArgLeuHisArgGlnLeuThrTyrAspLeuLeuProThrAspSerAlaGlnAspLeu :::               :::             :::             :::               :::                 :::	Qy 383 ABRGIYILETYPPOLEUMETABR		Qy 262 ThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArgHisSerLeuSer 281

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FILE REFERENCE: 00786/397003
CURRENT APPLICATION NUMBER: US/10/661,426
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR PILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 16
SOPTWARE: FRAELSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 1101
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Best Local Similarity:
Query Match:
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; ORGANISM: Arabidopsis thaliana
US-10-661-426-6
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  ATGAGTCCTGAGAGGATTAACACTGATTTGAATCAGGGAAAGTAT---GATGGTTATGCT
                                                                                                                                                                                                               IleGlySerValTrp---HisArgIlePheSerAsnAlaLeuArgProProThrAlaLeu
                                                                                                                                                                                                                                                                                               IleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLys 190
                                                                                                                                                                                                                                                                                                                                            GCTGATCTATCTCGTCAGATTCTTAGTGGTTTAGCTTATCTCCAT-----AGCCGTCAC
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                                              PheProProGlu-----
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                                                                                                                            ProAspAspLeuArgSerProIleArgAlaGluArgGluGluLeuArgAsnLeuHisPhe
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US-11-136-527-6476
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Best Local Similarity:
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LENGTH: 1400
TYPE: DNA
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: MOUNTS, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
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eAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuVal------
                                        TGTAGCCACAGGGCAGGAGGTGGCCATTAAACAGATGAACCTT--
                                                                              pThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAspArgLysAlaPh
                                                                                                                          CTTCGAGAAGATTGGACAAGGT------GCTTCAGGCACAGTGTACACTGCAATGGA
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APPLICANT: Leong, John M.
APPLICANT: Campellone, Kenneth G.
TITLE OF INVENTION: ESPFU NUCLEIC ACIDS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 07917-280001
CURRENT APPLICATION NUMBER: US/11/134,563
CURRENT FILING DATE: 2005-05-20
PRIOR APPLICATION NUMBER: US 60/573,600
PRIOR APPLICATION NUMBER: US 60/573,600
PRIOR APPLICATION NUMBER: US 60/573,600
PRIOR FILING DATE: 2004-05-20
NUMBER OF SEQ ID NOS: 26
SOPTWARE: FABLEEQ for Windows Version 4.0
SEQ ID NO 15
Alignment Scores:
                                 ; TYPE: DNA
; ORGANISM: Homo
US-11-134-563-15
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-11-134-563-15
                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/11134563 Publication No. US20050287569A1 GENERAL INFORMATION:
                                                                                        LENGTH: 1638
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    AlaValLeuGluIleGlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaAr 275

                                                                                                                                                                                                YMetCysAlaLeuGluMet-----
                                                                                          AGCCTTGTACCTCATTGCCACCAATGGG------ACCCCAGAA------
                  -----CTTCAGAACCCAGAGAAGCTGTCAGCTATCTTCCGGGACTTTCTGAA 1496
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Matches:
Conservative:
Mismatches:
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APPLICANT: Woeth
APPLICANT: Mounts, William M
ITILE OF INVENTION: Probe Arrays For Expression Pro
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2380
LENGTH: 2539
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Best Local Similarity:
Query Match:
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; ORGANISM: Rattus
US-11-136-527-2380
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rGlnIleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAs 175
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                                                    GACAGAAACC
                                                                                                                  GGGAGATGAGCTATGGGTTGTCATGGAATACTTGGCCGGAGGCTCCTTAACAGATGTGGT 1452
                                                                                                                                                                                                                                                                                      sAlaPheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuVal-- 97
                                                                                                                                                                                                                                                                                                                                                   aMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAspArgLy
                                                                                uLysLysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysTh 155
                                                                                                                                                   aCysAlaArgValllePhelleThrGluTyrValSerSerGlySerLeuLysGlnPheLe 135
                                                                                                                                                                                    GGAAAACCAAAACCCAAACATTGTGAAC-----TATCTGGACAGTTACCTTGT 1392
                                                                                                                                                                                                           -----AspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAl 115
                                                                                                                                                                                                                                                     -----CAGCAGCAGCCGAAGAAAGAACTCATTATTAATGAGATCCTGGTCATGAG 1344
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US-10-618-941-99 (1-507) x US-10-661-426-3 (1-1101)
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LENGTH: 1101
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                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Master Activators of Pathogen Responsive TITLE OF INVENTION: Genes FILE REFERENCE: 00786/397003
CURRENT APPLICATION NUMBER: US/10/661,426
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Arabidopsis thaliana
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CAATTGAAATGATTGAGGGGGAGCCCCCATACCTCAATGAAAACCCTTTTGAGAGCCCTTGT 1805
TCTAGTGGATCTGCGCCGTCTTCTGGTGGTTCGGCGTCTTCAACGAACACTAACAGCTCC 210
                                       AsnGlnGlyAsnMetProGlyLeuGlnSerThrPheLeuAlaMetAspThrGluGluGly 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----CTTCAGAACCCAGAGAAGTTGTCAGCTATTTTCCGGGGACTTTTTGAACCGCTGTC
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US-11-136-527-3130
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Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William M
APPLICANT: MOUNTS, WILLIAM M
APPLICANT: MOUNTS, WILLIAM M
APPLICANT: NOUNTS, WILLIAM M
APPLICANT: NOUNTS, WILLIAM M
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION UNMBER: US/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
NUMBER OF SEQ ID NOS: 362830
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SEQ ID NO 3130
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                                                                                          AlaCysSerProProIleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHis
                                                                                                                                 GATGAAGCGCAGATCGCAGCTGTGCAGAGAGTGTTTACAGGCGTTGGAGTTTTTACAT
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APPLICANT: Wyeth

APPLICANT: Mounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 2475

LENGTH: 2241
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Query Match:
DB:
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US-11-136-527-2475
; Sequence 2475, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               US-10-618-941-99 (1-507) x US-11-136-527-2475 (1-2241)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                               Local Similarity:
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APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO!
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOPTWARE: PatentIn version 3.2
SEQ ID NO 39
LENGTH: 2253
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US-10-770-726-39
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Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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; ORGANISM: Homo sapiens
US-10-770-726-39
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Pred. No.:
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                              246 PheSerPheGlyMetCysAlaLeuGluMetAlaValLeuGluIleGlnThrAsnGlyAsp 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 ValGluValValTrpAsnGlu------
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                                                              GACTACCTGCCCCCTGAAATGATTGAAGGTCGGATGCATGAT---GAGAAGGTGGATCTC
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CTTGGAACAGTTTATAGAGAACTTCAGAAACTTTCAAAGTTTGATGAGCAGAGAACTGCT
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TGGAGCCTTGGAGTTCTTTGCTATGAATTTTTTAGTTGGGAAGCCTCCTTTTGAGGCAAAC 1252
                                                                                                                               TCCAGGAGGACCACTCTC----
                                                                                                                                                                                                GAGCTTAAAATTGCAGAT------TTTGGGTGGTCAGTACATGCTCCATCT
                                                                                                                                                                                                                                                                                               SerProProIleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHisAsnGly 187
                                                                                                                                                                                                                                                                                                                              -----ACTTATATAACAGAATTGGCAAATGCCCTGTCTTACTGTCAT----- 1000
                                                                                                                                                                                                                                                                                                                                                 ArgAlaTrpLysArgTrpCysThrGlnIleLeuSerAlaLeuSerPheLeuHisAlaCys 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTTCCATGATGCTACC-----AGAGTCTACCTAATTCTGGAATATGCACCA 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrTrpLeuAspThrSerGluAlaCysAlaArgValIlePheIleThrGluTyrValSer 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGTCCCACCTTCGG---
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Search completed: January 14, 2006, 03:09:55 Job time : 407 secs

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Regult
No.
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-MODEL-frame+ p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool p/US10618941/runat 12012006 070206 14384/app query.fasta_1.647
-Q=/cgn2 1/USPTO_spool p/US10618941/runat 12012006 070206 14384/app query.fasta_1.647
-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bIts -START=1 -END=-1 -MATRIX=bLosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10618941 @CGN 1 1 1549 @runat 12012006 070206 14384
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodate/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodate/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodate/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodate/1/pubpna/US09B_PUBCOMB.seq:*

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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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US-10-425-114-26870

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US-10-812-71

US-10-175-523-117
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                 Sequence 33, Appl
Sequence 26870, A
Sequence 26848, A
Sequence 26873, A
Sequence 28974, A
Sequence 71, Appl
Sequence 117, App
                                                                                                                                                                                                              Description
Sequence 117,
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, Sequence 33, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: CAENEPEEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
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## ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                 Score:
                                                                             Pred. No.:
                                                                                        Alignment Scores:
US-10-618-941-99 (1-507) x US-10-618-941-33 (1-3765)
                                                                                                             US-10-618-941-33
                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                               2.99e-313
2670.00
100.00%
100.00%
100.00%
                               Conservative: Mismatches: Indels:
                                                                Length:
Matches:
                      3765
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SEQ ID NO 33 LENGTH: 3765

NUMBER OF SEQ ID NOS: 143 SOFTWARE: PatentIn version 3.2

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                                                                                                                                                                                                                                                                                                                                                                                          GlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArgHisSerLeu
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ProLeuGlnTrpArgTyrSerGluValSerPheMetGluLeuAspLysPheLeuGluAsp
                                           AAGACCAAGGCCATGGACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGCAGGCCC
                                                                  LysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeuProArgProArgArgPro
                                                                                                                      CTGGCAGCCCACTGCTTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTGGAGGAG
                                                                                                                                                 LeuAlaAlaHisCysPheIleGlnHisGlnTyrLeuMetProGluAsnValValGluGlu
                                                                                                                                                                                                                                ProSerAlaHisSerLeuLeuPheHisArgValLeuPheGluValHisSerLeuLysLeu
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Sequence 26870, Application US/10425114

Publication No. US20040034888A1

PublicANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cac, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 26870

LENGTH: 3837

TYPE: DNA
                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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FEATURE:
OTHER INFORMATION: Clo.
US-10-425-114-26870
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AAGCTCCTGGCAGCCCACTGCTTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTG
                                                                                   ArgArgProSerAlaH18SerLeuLeuPheH18ArgValLeuPheGluValH18SerLeu
                                                                                                                                                      SerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAlaArgAspProAla
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APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

SEQ ID NO 26848

SEQ ID NO 26848

LENGTH: 3838

TYPE: DATE
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Score:
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                                        US-10-618-941-99 (1-507)
                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Koralic, David K.
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26873
LENGTH: 3846
   Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-425-114-26873
                                                                                        Alignment Scores: Pred. No.:
                                                                                                                                             US-10-425-114-26873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26873, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                             OTHER INFORMATION: Clone
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                                          GluIleGlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArgHis
                                                                                     AspGlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMetAlaValLeu
                                                                                                                               AlaGluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGluValAla
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28974
LENGTH: 3128
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
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Ob 942 GCTGAGCGAGAGGAACTTCGGAACCTTCCTCCCCCCAGAGTATGGAGAGGTGGCC 1001  Qy 239 AspGlyThrAlavalAspIlePheSerPheGlyMetCysAlaLeuGluMetAlavalLeu 258	219 AlaGluArgGluGluLeuArgAsnLeuHisPheProProGluTyrGlyGluValAla 2	179 ASDThrIlePhelleGlnHisAsnGlyLeulleLySlleGlySerValTrpHisArgIle 19	Qy 159 SerālaLeuSerPheLeuHisālaCysSerProProIleIleHisGlyAsnLeuThrSer 178	Qy 149158	Qy 148 148  Db 660 GGGGCTGGGCGAGGATGCGGGGGCGGGCTCCGCAGCCCTCTCCTGCGCCCACC 719	Db 600 ACGGGGTTGGGGCAGCCTCGGGGACTGGGATGGTGAGGGGGGTGCCCGGCCGCCTCGGACA 659	141 AsnHisLysAlaMetAsnAlaArg14	Qy 121 PheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLysLys 140	Qy 101 AsmīlevallysLeuHislysTyrTrpLeuAspThrSerGluAlaCysAlaArgVallle 120	Oy 81 AlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuValAspHisPro 100	Qy 61 ThrGluGlyValGluValValTrpAsnGluLeuHisPheGlyAspArgLysAlaPhe 80	Qy 41 ArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPheLeuAlaMetAsp 60	Qy 21 GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg 40	Qy 1 MetAlaAlaProGluProAlaProArgArgAlaArgGluArgGluArgGluArgGluAsg 20	Score: 2531.50 Matches: 499 Percent Similarity: 83.47% Conservative: 1 Best Local Similarity: 83.31% Mismatches: 1 Query Match: 94.81% Indels: 99 DB: 7 Gaps: 3 US-10-618-941-99 (1-507) x US-10-425-114-28974 (1-3128)
CURRENT APPLICATION NUMBER: US/10/840,512 ; CURRENT FILING DATE: 2004-05-07 ; PRIOR APPLICATION NUMBER: 60/469,014 ; PRIOR FILING DATE: 2003-05-09 ; NUMBER OF SEQ ID NOS: 239 ; SOFTWARE: Patentin version 3.2 ; SEQ ID NO 71	1	-51; e 71 tior	Db 1841 ATGAAGCTGGCCGCCTTCCTGGAGAGCACCTT	Db 1781 GCACGGGGCAGGCCGCCCCTCCGTCCCCCC	1722 CA	1662	ь	Db 1542 GAGCCCTTTGACTCTGAGACCAGAAAGGTCAT	1482	379 1422 300	1362	1302	1242	Ov 319 LvsLeuLeuLalaslaslaslaslaslaslaslaslaslaslaslaslas	1062 279 1122

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; TYPE: DNA
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   SerAspProAsnMetArgGluPheIleLeuCysCysLeuAlaArgAspProAlaArgArg
                                          GlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArgHisSerLeu
                                                                                          ThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMetAlaValLeuGluIle
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, Jeffrey
APPLICANT: Hook, Derek
APPLICANT: Klimczak, Leszek
APPLICANT: Laeng, Pascal
APPLICANT: Laeng, Pascal
APPLICANT: Palfreyman, Michael
APPLICANT: Laeng, Pascal
APPLICANT: Palfreyman, Michael
APPLICANT: Rajan, Prithi
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/17/95-US3
CURRENT APPLICATION NUMBER: US 60/299,151
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/299,151
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR APPLICATION NUMBER: US 60/349,936
PRIOR APPLICATION NUMBER: US 60/361,834
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US-10-175-523-117
; Sequence 117, Application
; Publication No. US20030096
; Publication No. US20030096
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; PRIOR FILING DATE: 2002-03-04; NUMBER OF SEQ ID NOS: 197; SOFTWARE: PatentIn version 3.1; SEQ ID NO 117; LENGTH: 3538; TYPE: DNA; ORGANISM: Homo sapiens
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US-11-099-266-117
US-11-099-266
; Sequence 117, Application US/11099266
; Publication No. US20050181433A1
; GENERAL INFORMATION:
   APPLICANT: Evokman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Hook, Derek
; APPLICANT: Laeng, Pascal
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Palfreyman, Michael
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APPLICANT: Laeng, Pascal
APPLICANT: Palfreyman, Michael
APPLICANT: Rajan, Prithi
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS
FILE REFERENCE: 03235/100J795-US4
CURRENT APPLICATION NUMBER: US/11/099,266
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: US 10/175,523
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,151
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PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR APPLICATION NUMBER: US 60/349,936
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 60/349,936
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/361,834
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PRATENTIAN OF SEQ ID NO 117
LENGTH: 3538
TYPE: DNA
ORGANISM: Homo sapiens
US-11-099-266-117
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             SerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArg
                                                         LeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeuThr
                                                                                        ACCCGACCGACGGAGTCGTGCGTCCGCCAGGCCTGGAAGCGCTGGTGCACGCAGATC
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87.17%
86.79%
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Matches:
Conservative:
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RESULT US-09-8 Seque Paten APPL APPL TITL FILE CURR	g Qy	Qу	Qγ	D Qy	Db Qy	рь	Qy .	p Q	pb Qy	ДУ	D Qy	Db Qy	D 9	D Q	D Q	₽ <b>Q</b>
ESULT 9 S-09-862-027-9 S-09-862-027 Sequence 9, Application US/09862027 Patent No. US20020142428A1 GENERAL INFORMATION: APPLICANT: Hodge, Martin R. TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof FILE REFERENCE: 35800/234862 CURRENT APPLICATION NUMBER: US/09/862,027	498 ThrPheLeuLysTyrArgGlyThrGlnAla 507	478 ValHisTyrGlyPheLeuHisGluAspAspArgMetLysLeuAlaAlaPheLeuGluSer 497	458 ArgGlnLeuThrTyrAspLeuLeuProThrAspSerAlaGlnAspLeuAlaSerGluLeu 477	438 SerGluAspLysAlaArgTrpHisLeuThrLeuLeuLeuValLeuGluAspArgLeuHis 457	418 ProGluProPheAspSerGluThrArgLysVallleGlnMetGlnCysAsnLeuGluArg 437	398 GlyLeuProArgValLeuAlaProProBroGluGluValGlnLysAlaLysThrProThr 417	378 LeuGluAspValArgAsnGlyIleTyrProLeuMetAsnPheAlaAlaThrArgProLeu 397 	358 ArgArgProProLeuGlnTrpArgTyrSerGluValSerPheMetGluLeuAspLysPhe 377	338 ValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeuProArgPro 357	318 LeuLysLeuLeuAlaAlaHisCysPheIleGlnHisGlnTyrLeuMetProGluAsnVal 337	298 AlaArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGluValHisSer 317 	278 HisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAlaArgAspPro 297	258 LeuGluIleGlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArg 277 	238 AlaAspGlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMetAlaVal 257 	218 ArgAlaGluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGluVal 237	198 IlePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerProIle 217              661 ATCTTCTCCAATGCACTTCCAGATGATCTCCGAAGCCCCATC 702

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PRIOR APPLICATION NUMBER: US 09/345,47
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 981

TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(981)
OTHER INFORMATION: n=A,T,C o
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                                                           AsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerProIleArgAlaGlu
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CGAGAGGAACTTCGGAACCTGCACTTCTTCCCCCCAGAGTATGGAGAGGTGGCCGATGGG
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APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: Novel Kinases and Uses The TITLE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/10/989,228
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US/09/862,027
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
PRIOR PRIOR HOPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOPTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 981
TYPE: DNA
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Publication No. US20050089917A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature LOCATION: (1)...(981)
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RESULT 11
US-09-840-787-69
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Patent No. US20020058264A1
GENERAL INFORMATION:
                                                                Yue, Henry
Guegler, Karl J.
Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
RUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                         APPLICANT: Lal, Preeti
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                                 CITY: Palo Alto
STATE: CA
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   COUNTRY: USA
ZIP: 94304
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Bandman, Olga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/840,787
FILING DATE: 23-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/518,865
FILING DATE: <Unknown>
ATTORNEY/AGBUT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELEPHONE: 415-845-4166
TELEPLY. 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: BRAITUT03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRACTSCO FOR WINDOWS VERSION
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                      IleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeu 176
                                                                                     LysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTzpLysArgTzpCysThrGln
                                                                                                                                  GCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAAG
                                                                                                                                                    AlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys
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ATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCATCATCCATGGGAACCTG
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity:
Query Match:
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APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
APPLICANT: MATSUDA, Akio
APPLICANT: MIRAMATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
CUURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR PILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: UP 2001-157043
PRIOR APPLICATION NUMBER: UP 2001-260681
PRIOR APPLICATION NUMBER: UP 2001-313175
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
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; LOCATION: (113)..
US-10-153-668-321
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ORGANISM: Homo
FEATURE:
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                      IleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeu
                                                                                                 LysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln
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ATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCCATCATCCATGGGAACCTG
                                                                           AAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACAA
                                                                                                                                                          GCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAAG
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RESULT 12
US-10-153-668-321
; Sequence 321, Application US/10153668
; Publication No. US20030092616A1

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RESULT 13
US-10-687-553A-882
; Sequence 882, Application US/10887553A
; Publication No. US20050085436A1
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                                                                                                                                                                                                                               GluAsnValValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeu 354
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                                                                     CAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTC
                                                                                         ArgMetLysLeuAlaAlaPheLeuGluSerThrPheLeuLysTyr 502
                                                                                                                                          AspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAsp
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                                                                                                                                                                           CTTCTGCTGAAGTTGGAGGACAAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAAT 156
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APPLICANT: Garza, Dan
APPLICANT: Li, Hao
TITLE OF INVENTION: wethod to treat conditions associated
TITLE OF INVENTION: with insulin signalling dysregulation
FILE REFERENCE: 4-33262
CURRENT APPLICATION NUMBER: US/10/887,553A
CURRENT FILING DATE: 2004-07-08
PRIOR APPLICATION NUMBER: 60/485,883
PRIOR APPLICATION NUMBER: 60/485,883
PRIOR FILING DATE: 2003-08-07
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 882
LENGTH: 2163
TYPE: DNA
ORGANISM: human
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: MOUNTS, WILLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED VITILE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 1845
LENGTH: 2163
TYPE: DNA
ORGANISM: Homo sapiens
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37	17 GluArgGluAspGluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArg	57.47% Indels: 3 Gaps: 7) x US-09-764-875-151 (1-2225)	Fred. No.: 2.6.be-175 Length: 2225 Score: 1534.50 Matches: 305 Percent Similarity: 73.54% Conservative: 59 Best Local Similarity: 61.62% Mismatches: 102		מ	; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 151 ; LENGTH: 2225 ; TYPE: DNA	CURRENT FILING DATE: 2001-0 Prior application data remov NUMBER OF SEQ ID NOS: 1249	FILE REFERENCE: PUZO2  CURRENT APPLICATION NUMBER: US/09/764 875	GENERAL INFORMATION: APPLICANT: Rosen et al.	RESULT 15 US-09-764-875-151 ; Sequence 151, Application US/09764875 ; Publication No. US20040018969A1	Db 1622 CAGAGCCGGTTGACTTCTCTCGCTAGAAGAAGACCTTGAACAAGTTC 1666		468 AspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAsp	QY 448 LeuLeuValLeuGluAgpArgLeuHisArgGlnLeuThrTyrAspLeuLeuProThr 467                ::           ::	428 VALLIEGIIMPECGIICYSASHLEUGIIARGSETGIIASDLYSALAARGTTPHISLEUThr	1382 GTCGTGCCCCCTCTGTCAAGACTCCGAACCTGAACCAGCTGAGGTGGAGACTCGCAAG	1334	Qy 394 ThrArgProLeuGlyLeuProArgValLeuAlaProProProGluGluVal 410	Db 1280 TTAGATAAATTCCTTGAAGATGTCAGGAATGGGATCTATCCTCTGACAGCCTTT 1333	Qy 374 ΓεμλερίγεΡηεΓευGluAspValArgAsnGlγIleTyrProΓεμΜετΑsnPheAlaAla 393	OY 355 PTOATGPROATGARGPROPROLEUGINTRPARGTYRSERGIUVAISERPHEMELGIU 373	1160 GAGAACGCT	
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394 ThrargProLeuGlyLeuProArgValLeuAlaProProProGluGluVal 410	374 LeuAspLysPheLeuGluAspValArgAsnGlyTleTyrProLeuMetAsnPheAlaAla 393 	355 ProArgProArgArgProProLeuGlnTrpArgTyrSerGluValSerPheMetGlu 373	335 GluAsnValValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeu 354        :::	1128 GTGCCCTCGCTCAAACTCCTTGCGGCCCACTGCATTGTGGGGACACCAACACATGATCCCA 1187	315 ValHisSerLeuLysLeuLeuAlaAlaHisCysPheIleGlnHisGlnTyrLeuMetPro 334	295 ArgAspProAlaArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGlu 314	273 ATSATAMASHINSSTLEUSETABPTOABHMECATGGIVERETIELEUCYSCYSLEUAIA 294 1008 AGTGCCATCCAGCTTCTAGAAGACCCATTACAGAGGGAGTTCATTCA	GCAGTGCTGGAGATTCAGGGCAATGGAGAGTCCTCATATGTGCCACAGGAAGCCATCAGC		237 ValalaaspGlyThralaValaspIlePheSerPheGlyMetCysalaLeuGluMet 255 	828 GTGAAGACTTGTCGAGAAGAGCAGAAGAATCTACACTTCTTTGCACCAGAGTATGGAGAA 887	GCTCCTGACACTATCAACAATCAT	197 ArgIlePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerPro 216	177 ThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHis 196	157 IleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeu 176 	137 LysThrLysLysAsnHislysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln 156 		117 AlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys 136			77 ArgLysAlaPheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeu 96	390 CTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGGAATGAGGTACAGTTCTCTGAA 449	

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-Q=/cgn2_1/USPTO_spool_p/US10618941/runat_12012006_070203_14258/app_query.fasta_1.647
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polynucleotide sequence is a human kinase DNA sequence
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                                                                                                                                GlyPheLeuHisGluAspAspArgMetLysLeuAlaAlaPheLeuGluSerThrPheLeu
                                                                                                                                                                                    ThrTyrAspLeuLeuProThrAspSerAlaGlnAspLeuAlaSerGluLeuValHisTyr
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                                                                                                                                                                                                                                                                                                                                     CGTGTGCTGGCCCCACCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAGCCC
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  standard;
                                                                                                             GGCTTCCTCCACGAGGACGACCGGATGAAGCTGGCCGCCTTCCTGGAGAGCACCTTCCTC
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CC differentially expressed in response to steroid treatment. Also included care the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high comparison of screening molecules or compounds to identify a cligand that specifically binds a cDNA. The sample is from a subject with cc disease. The high throughput method of screening molecules or compounds to identify a condentify a ligand that specifically binds a cDNA. The sample is from a subject with cc disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises: combining the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and at least one molecule or compound. The molecules or compounds are regulatory proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis. The present sequence represents a human cDNA which is differentially expressed in steroid-induced C3A liver cells. Note: The specification but was obtained in electronic format directly from USPTO or at sequence .html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises CDNAs that are differentially expressed in response to steroid
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                              GTCAGGAATGGAATCTACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTGCCC
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ArgValLeuAlaProProFluGluValGlnLysAlaLysThr-ProThrProGluPr 420
                                                   ValArgAsnGlyIleTyrProLeuMetAsnPheAlaAlaThrArgProLeuGlyLeuPro
                                                                                                             ProLeuGlnTrpArgTyrSerGluValSerPheMetGluLeuAspLysPheLeuGluAsp
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        The invention describes a polynucleotide consisting
                                                                                                                                                             New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathogo pests, for conferring increased resistance to plant disease, or for
                                                                                        Claim 1;
                                                                                                                                                                                                                                                                           WPI; 2004-180133/17
                                                                                                                                                                                                                                                                                                                                Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZHOU/)
(KOVA/)
(SCRE/)
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KOVALIC D K.

SCREEN S E.

TABASKA J E.

CAO Y.
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     recombinant DNA construct of a sequence encoding an
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CC available in electronic form from the US patent office at CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide CC of the invention are also useful in physical arrays of molecules and as CC plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme CC osmotic conditions, pathogens or pests, for manipulating growth rate in CC plant cells by modification of the cell cycle pathway, for conferring CC increased resistance to plant disease, for producing galactomannan, CC lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake CC or by providing improved plant growth and development under at least one Stress condition or for modifying seed oil or protein yield and/or CC content. This sequence represents a plant full length insert
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Sequence 3837 BP; 799 A; 1195 C; 1084 G; 759 T; 0 U; 0 Other;

Query Match: DB:

Percent Similarity: Best Local Similarity:

2.09e-250 2584.00 88.05% 88.05% 96.78%

Length: Matches: Conservative: Mismatches: Indels:

Gaps:

No . :

Scores:

밁 ð 음 성 밁 Ś 밁 S 밁 S 밁

068	CGACCGACGGAGTCGTGCGTCCGCCGCCAGGCCTGGAAGCGCTGGTGCACGCAGATCCTG	Db 831	D
158	AlaTrpLysArgTrpCysThrGlnIleLeu	ly 149	ð
830	GGGGCTGGGCGAGGATGCGGGGCGGGCTCCGCAGGCCCAGCCGCCTCTCCCTGCGCCCACC	)b 771	멍
148		)y 148	Ş
770	ACGGGGTTGGGGCAGCCTCGGGGACTGGGATGGTGAGGGGGGTGCCCGGCGGCCTCGGACA	)b 711	밁
148		Qy 148	Ø
710	AACCACAAGGCCATGAACGCCCGGGTATGGGGAGCGGGCTGGGGCAGCCACGGGGACAGG	)b 651	엉
148		Qy 141	ю
650		Db 591	0
140	PheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLysLys	ly 121	S
590	ACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTCATC	Db 531	ט
120	AsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCysAlaArgValIle	Qy 101	ю
530	GCGGCGCACGAGGAAGATCCAGACCGTGTTCGAGCAGCTGGTGCTGGTGGACCACCCG	Db 471	b
100	-	Qу 81	Ø
470	ACGGAGGAGGGGTAGAGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCCCTTC	Db 411	Ð
80	ThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAspArgLysAlaPhe	Qy 61	0
410		Db 351	U
60	ArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPheLeuAlaMetAsp	Qy 41	ρ.
350		Db 291	U
40	GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg	Qy 21	o.
290		Db 231	U
20	MetAlaAlaProGluProAlaProArgAlaArgGluArgGluArgGluArgGluArgGluAsp	Qy 1	Ø
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TTCCTCAAGTACCGTGGGACCCAGGCC 1919
                           PheLeuLysTyrArgGlyThrGlnAla 507
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                                                                                                                 HisTyrGlyPheLeuHisGluAspAspArgMetLysLeuAlaAlaPheLeuGluSerThr
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The invention describes a recombinant DNA construct comprising a CC polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide CC of the invention are also useful in physical arrays of molecules and as CC plant breeding markers. The recombinant DNA construct is useful for CC improving plant tolerance to cold, heat, drought, herbicides, extreme CC compartic conditions, pathogens or pests, for manipulating growth rate in CC plant cells by modification of the cell cycle pathway, for conferring CC increased resistance to plant disease, for producing galactomannan, CC recombination in plants, for improving yield by modification of conferring CC increased resistance to plant disease, for producing galactomannan, CC recombination in plants, for improving yield by modification of plant growth and development under at least one of provoviding improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
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                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 26848; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3846
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The invention describes a recombinant DNA construct comprising
                                                 Claim 1;
                                                                                               New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathoge pests, for conferring increased resistance to plant disease, or for improving yield.
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05-NOV-2001;
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cc polynucleotide consisting of a sequence encoding an amino acid sequence cavailable in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide cof the invention are also useful in physical arrays of molecules and as improving plant tolerance to cold, heat, drought, herbicides, extreme combinitions, pathogens or pests, for manipulating growth rate in conditions, pathogens or pests, for manipulating growth rate in increased resistance to plant disease, for manipulating growth rate in collinor conditions, pathogens for increasing the rate of homologous concerns or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of contents or carbohydrate, nitrogen or phosphorus use and/or uptake continuition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert of the invention.
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Sequence 3128 ₽P; 617 A; 973 Ç 966 <u>ი</u> 572 Ή. 0 U; 0 Other;

Best Local S Query Match:

Percent Similarity: Best Local Similarity:

3.17e-245 2531.50 2531.47% 83.47% 83.31% 94.81%

Length:
Matches:
Conservative:
Mismatches:
Indels:

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WO2005000200-A2

07-MAY-2004; 2004WO-US014421.

09-MAY-2003; 2003US-0469014P

(SUGE-) SUGEN INC

Caenepeel S, Manning ō Charydczak G, Grigoriev

P-PSDB; 2005-066508/07. ADV97865

New isolated, enriched, or purified kinase nucleic acids and polypeptides, useful for diagnosing or treating, e.g. cancers, neurological and neurodegenerative diseases, cardiovascular dinflammatory disorders. disease,

ID NO 300pp; English.

This invention relates to novel isolated, enriched or purified nucleic cald molecules that encode kinase polypeptides. Specifically, it refers to a bioinformatics strategy used to identify mammalian members of the correct and lipid kinase families. The present invention provides methods correct and lipid kinase families. The present invention provides methods correct in a substance that modulates the activity of a kinase correct correction in a sample as a diagnostic tool for a disease or disorder.

CC Purthermore, it describes generation of a knock-out mouse whose genome is corrected by recombination at a nucleic acid sequence such that it corrected by recombination at a nucleic acid sequence such that it corrected by recombination at a nucleic acid sequence such that it corrected by recombination at a nucleic acid sequence such that it corrected by recombination at a nucleic acid sequence such that it corrected by recombination at a nucleic acid sequence such that it corrected by recombination at a nucleic acid sequence such that it corrected by recombination are useful for the diagnosis and treatment of cancer, corrected not previous system diseases, psychotic and neurological disorders, neurodegenerative diseases, metabolic disorders, they can be considered therapy purposes and compositions exhibit cytostatic, antimigraine, analgesic, endocrine-Gen., nootropic, tranquilizer, corrected, open that moderate and protective, antiparkinsonian, virucide, fungicide, antibacterial, antidiabetic, anorectic, antiarteriosclerotic, cophibalmological, antiallergic and gastrointestinal-gen. This column to that encodes a murine protein kinase of column column by the column column column column.

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AAF44681 standard; CDNA; 3304

AAF44681;

Novel protein kinase cDNA, 27-MAR-2001 (first entry) SEQ ID ĕ

61.

Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; immunosuppressive; cardiant; renal; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a novel protein kinase. The nucleic acids CC and the protein kinases they encode may be used in the treatment and CC diagnosis of diseases associated with inappropriate kinase expression CC such as immune-related diseases and disorders, cardiovascular disease, CC neurodegenerative diseases and/or cancers. The nucleic acids and CC complementary sequences may also be used as DNA probes in diagnostic CC assays. The kinase polypeptides may be used as antigens in the production CC of antibodies of kinase expression and activity. Anti-kinase antibodies CC antibodies of kinase expression and activity. Anti-kinase antibodies CC expression and activity. Diseases related to kinase expression and CC activity include rheumatoid arthritis, atherosclerosis, autoimmune CC disorders, complications of organ transplantation, myocardial infarction, CC inflammatory powel disease, chronic inflammatory bowel disease, chronic confiammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, alterosis, asthma, osteoarthritis, alterosis, and reproductive discoars, rhinitis, autoimmunity, diabetes, cancers and reproductive
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                                                                                                                                                                                                                                                                                                                                                                                            US-10-618-941-99 (1-507) x ADI29379
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a compound comprising a sequence comprising 8-80 base pairs (Dp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3), that specifically hybridises with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated CDNA included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                                                                                  No.:
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 233pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-2002; 2002US-00174319
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MAP/microtubule affinity-regulating kinase 3; cancer;
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                               CTGACCTACGACCTGCTCCCAACGGACAGCCCCAGGACCTCGCCTCGGAGCTCGTGCAC 1302
                                                                                        GACAAGGCGCGCTGGCATCTCACTCTGCTTCTGGTGCTGGAAGACCGGCTGCACCGGCAG
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                                              LeuThrTyrAspLeuLeuProThrAspSerAlaGlnAspLeuAlaSerGluLeuValHis 479
                                                                                                          AspLysAlaArgTrpHisLeuThrLeuLeuLeuValLeuGluAspArgLeuHisArgGln
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Alignment
                                                                                    This invention relates to a novel screening method identified as a multice parameter high throughput screening (MPHTS) assay. Specifically, it crefers to an assay that utilises the disease signature of a plurality of specific genes associated with a particular disease, and identifies confict that disease and those chals taken from individuals conference by that disease and those that are not affected. The present invention then describes the screening of candidate pharmaceutical compounds to identify those that have a potential therapeutic benefit for the treatment of neuropsychiatric and neurodegenerative disorders concluding schizophrenia, bipolar affective disorder (BAD) and autism, as concluding schizophrenia, bipolar affective disorder (BAD) and autism, as concluding schizophrenia, bipolar affective disorder (BAD) and autism, as concluding schizophrenia, bipolar affective disorder (BAD) and autism, as concluding schizophrenia, bipolar affective disorder (BAD) and autism, as concluding schizophrenia, bipolar affective disorder (BAD) and autism, as concluding schizophrenia, and altidepressant. Furthermore, the screening concurrence of and antidepressant. Furthermore the screening compounds may be rapidly screened with a minimal amount of labour and compound confort. This polymucleotide is the cDNA sequence of a gene that is conformed conformed in an exemplification of the invention.
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14-NOV-2001;
18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a compound that can treat disease or disorders, such neuropsychiatric disorder e.g., schizophrenia, or autism, compris determining the expression of one or more efficacy genes in a cel contacted with the test compound.
                                        Sequence 3538 BP;
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07-SEP-2001;
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2001US-0325150P.

2001US-033047P.

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and/or NRBP function. Preferred NRBP-modulating agents specifically bind to NRBP polypeptides and restore RAC function. Other preferred NRBP-modulating agents are nucleic acid modulators such as antisense oligomers and RNAi that repress NRBP gene expression or product activity. NRBP modulating agents may be evaluated by in vitro or in vivo assay for molecular interaction with an NRBP polypeptide or nucleic acid. Agents that produce a change in the activity of there assay system relative to controls are identified as candidate RAC modulating agents. The assay system may be cell-based or cell-free. NRBP modulating agents include NRBP-related proteins (e.g. dominant negative mutants and biotherapeutics), NRBP-specific antibodies, NRBP-specific antisense oligomers and other nucleic acid modulators, and chemical agents that specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind to or interact with NRBP or compete with an NRBP specifically bind specifically bind
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                                                                                                         binding partner. The screening assay may be an apoptosis assay, a cell proliferation assay, an angiogenesis assay or a hypoxic induction assay. A method for diagnosing a disease, especially cancer, in a patient uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a candidate RAC pathway modulating agent using a nuclear receptor binding protein (NRBP) polypeptide or nucleic acid, useful for diagnosing or treating cancer.
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P-PSDB; AEA61759.
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3538 BP; 806 A; 1076 Ç 928 ດ 728 'n, 0 U; O Other;

probe for NRBP expression.

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Percent Similarity:
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                                                                     ProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCysAlaArgVal 119
                                                                                                                           PheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValAepHis 99
               IlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLys 139
                                                      CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTC
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SerGluAspLysAlaArgTrpHisLeuThrLeuLeuLeuValLeuGluAspArgLeuHis
                                                                                  ProGluProPheAspSerGluThrArgLysValIleGlnMetGlnCysAsnLeuGluArg
                                                                                                                                 GGGCTGCCCCGTGTGCTGGCCCCACCCCCGGAGGAGGTCCAAAAAGGCCAAGACCCCGACG
                                                                                                                                                      GlyLeuProArgValLeuAlaProProProGluGluValGlnLysAlaLysThrProThr
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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P-PSDB;
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Ma Y,
                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1404-1406; 6221pp;
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Y, Zhao QA, W
Yang Y,
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DB; AAM78691.
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                                                  treatment immune, in disorders
                                                                 The present invention relates to human protein kinase. The proteins are from new human genes termed h12832, h14138, h14833, h15990, h15993, h16341 and h2252. The proteins may be used to identify modulators of their activity. The proteins may also be used to derive products for the treatment of cellular growth related disorders, malignancies, cancers, immune, inflammatory, respiratory, haematological and bone-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; protein kinase; cell growth; tumour; respiratory; haematological; bone disorder;
                                                                                                                                                                                                                                                                                        New protein kinase polypeptides, nucleic acids and anti-kinase antibodies, useful for diagnosing and treating e.g. cancer, inflammatory, immune, cardiovascular and bone disorders.
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                                                                                                   GlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArgHisSerLeu
                                                                                                                                                                                                   ArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGluValAlaAspGly
ProSerAlaHisSerLeuLeuPheHis-ArgValLeuPheGluValHisSerLeuLysLe
                                                   SerAspProAsnMetArgGluPheIleLeuCysCysLeuAlaArgAspProAlaArgArg
                                                                                     CAGACCAATGGGGACACCCGGGTCACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTG
                                                                                                                                                    ThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMetAlaValLeuGluIle
                                                                                                                                                                                                                                                   AsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerProIleArgAlaGlu
                                                                                                                                                                                                                                                                                     ATCTTCATTCAGCACAACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTCTCC
                                                                                                                                                                                                                                                                                                  | IlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArgIlePheSer
                                                                                                                                                                                                                                                                                                                                     CTCAGCTTCCTGCACGCCTGCAGCCCCCCAATCATCCACGGGAACCTGACCAGCGACACC
                                                                                                                                                                                                                                                                                                                                                   LeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeuThrSerAspThr
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RESULT 14
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                                                                                           Cl length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the Complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence of complementary to a polynucleotide which comprises a 5'-end sequence, where the coligonucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence's end sequence omplementary to a polynucleotide comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in the comprises at least 15 nucleotides and the combination of the specification. The primers are useful for synthesising polynucleotides, comparation and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs as allow obtaining of the full-length cDNAs as allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and comparation and an amino acid sequences; and AAH13629 to AAH13632 represent coligonucleotides, all of which are used in the exemplification of the present of the comprise of the
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length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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P-PSDB; ABB05696.
                                                                            Human cDNA sequences and clones derived from human fetal brain, kidney, melanoma, testis and amygdala cDNA libraries, useful in
                                                                                                                                                                                                                                                                                                                                                                       Human; foetal brain; foetal kidney; melanoma;
                                                                                                                                                                                                                      25-APR-2000; 2000US-0199380P
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                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA93734 standard;
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The present invention describes assemblages and computer comprising novel human cDNA sequences and clones derived

readable media from human

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Page 215-216; 611pp; English

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## ALIGNMENTS

ACCESSION VERSION KEYWORDS RESULT 1 BC068117 LOCUS SOURCE ORGANISM REFERENCE DEFINITION AUTHORS Strauberg, R. L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., BC068117 BC068117.1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 3163) Mus musculus BC068117
3163 bp mRNA linear HTC 08-FEB-200
Mus musculus nuclear receptor binding protein 2, mRNA (cDNA clone Mus musculus (house mouse) IMAGE: 6419290). GI:45829694 HTC 08-FEB-2005 Ġ

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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

1 (bases 1 to 3729)
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                                                                Submitted (04-SEP-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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    oProIleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHisAsnGlyLeuIl 189
                                                CTGGAAGCGCTGGTGCACGCAGATCCTGTCTGCGCTCAGCTTCCTGCACGCCTGCAGCCC
                                                                         aTrpLysArgTrpCysThrGlnIleLeuSerAlaLeuSerPheLeuHisAlaCysSerPr
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                                                                                                                                  AGGCCCAGCCGCCTCTCCCGCCCCACCCGACCGACGGAGTCGTGCGTCCGCCGCCAGGC
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/clone Tib="NIH MGC_115"
/lab host="DH10B"
/note="Vector: pCMV-SPORT6'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/db_sinder:5180619"
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2037.50
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ValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCys 116 :::::	ArgLysAlaPheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeu 96	LeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAsp 76	TrpGlnLygArgGluGlnValAgnGlnGlyAgnMetProGlyLeuGlnSerThrPhe 56	∍pGluSerGlu! ::         NAGAAAGTGAA(	58.52% Indels: 4 Gaps: 7) x AK046142 (1-2163)	7.4le-155 Length: 2163 1562.50 Matches: 310 : 74.75% Conservative: 60	/note="putative"	EADQSRLSSVLEETLNKFNFSRNSTLNTATVTVSVVELT" 2144 .2149 /note="putative" 2163	MAVLEIQGNGESSYVPOEAISSAIQLLEDSLOREFIQKCLQSEPARRPTARELLEHPA LPEVPSLKLLAHCIVGHQHMIPENALEEITKMDTSAVLAEIPAGPGREPVOTLYSQ SPALELDKFLEDVRNGIYPLTAFGLPRPQOPQQEEVTSPVVPPSVKTPTPEPARVETR KVVLMQCNIESVEBGVKHHLTLLKLEDKLNRHLSCDLMPNESIPDLAAELGQLGFIS	EEEESSELEESPOGRWQKKREEVNQRINVEGIDSAYLAMDTEEGVEVVMINERGES EERKYKLQEEKVRAVEDILIQLEHLAIVKEHKYWADVKENKAAVIFITEVMSSGSLKQ FLKKTKKNHKTWNEKAWKRWCTQILSALSYLHSCDEPIIHGALTCDTIFIQHNGLIKI GSVEHRIEANVAPDTINNHVKTCREEKKNLHEBAPEYGEVTTVTTVTTYSTOKTALE	/Codon Btart=1 /Codon Btart=1 /Codon Id="BAC32612.1" /proteIn id="BAC32612.1" /db_xref="GI:26337853" /translation="MARGRESCOTYVYSGSDPKVESSSTAPGI.TGVSPPVTSTTSAASPE	RECEPTOR BINDING PROTEIN (HLS7-INTERACTING PROTEIN KINASE) homolog [Mus musculus] (SPTR Q99J45, evidence: FASTY, 97.8%ID, 99.8%length, match=1626) putstive"	/clone_Tib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 99. 17742 /norse="unnamed protein product, cIMITAD TO MICIERO"	/db_xref="taxon:10990" /clone="8230344117" /sex="male" /tissue type="corpora quadriqemina"	/organism="Mu8 musculu8" /mol type="mRNA" /strain="C57BL/60" /db_xref="FANTOM_DB:B230344L17"	riken.jp riken.jp ifiers	Encyclopedia Projected and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.  Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  Please visit our web site for further details.	MOISE
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448 LeuLeuLeuValLeuGluAspArgLeuHisArgGlnLeuThrTyrAspLeuLeuProThr 467                :::   :::       :::		GTTGTGCCCCCCTGTCAAGACTCCAACCTCCTGAGCCAGCTGAAGTGGAGACACGAAAG	ThrargproLeuclyLeuproArgValleuAlaproProProProLuciuVal	LeuAspLysPheLeuGluAspValArgAsnGlyIleTyrProLeuMetAsnPheAlaAla	355 ProArgProArgArgProProLeuGlnTrpArgTyrSerGluValSerPheMetGlu 373	GluasnValValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeu        :::                   GAGAACGCTCTAGAGGAGATCACCAAGAACATGGATACCAGTGCTGTACTAGCTGAAATT	315 ValHisSerLeuLysLeuLeuAlaAlaHisCysPheIleGlnHisGlnTyrLeuMetPro 334	295 ArgAspProAlaArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGlu 314 	275 ArgAlaArgHisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAla 294	256 AlaValLeuGluIleGlnThrAsnGlyAspThrArgValThrGluGluAlaIleAla 274	237 ValAlaAspGlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet 255	217 IleArgAlaGluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGlu 236	197 ArgIlePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerPro 216	177 ThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHis 196 		137 LysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln 156 	468 CHGGAACAICHTAACAITGIAAGITHCACGAAIATTIGGGCIGAIGITAAAGAGAACAAG 527 117 AlaargValllePhelleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys 136	

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Mus musculus
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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                 CTGGCCATGGATACAGAGGAAGGTGTGGGAGGTTGTGTGGAATGAGGTACAGTTCTCTGAA
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                             GTTGTGCCCCCCTCTGTCAAGACTCCAACTCCTGAGCCAGCTGAAGTGGAGACACGAAAG
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                                              -----GlnLysAlaLysThrProThrProGluProPheAspSerGluThrArgLys
                                                                                                                  ThrArgProLeuGlyLeuProArgValLeuAlaProProProGluGluVal-----
                                                                                                                                                                                                            CCCGCAGGGCCAGGACGAGAACCAGTTCAGACTTTGTACTCTCAGTCACCAGCCCTAGAA
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Olagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKPZp43412411) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp43412411
Further information about the clone and the sequencing project if
available at http://mips.gsf.de/projects/cdna/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Fobo,G., Han,M. and Wiemann,S.
The German cDNA Consortium
Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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             /gene="DKFZp43412411"
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/codon_start=1
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LDKFILDVRNGIYFLMNFAATREJGLFRVLAFPEEEVQKAKTFTEEFFDSSTTRKVIGW
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/clone_Tib="434 (synonym: htes3
DH10B; sites NotI + SalI"
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/note="hypothetical protein (Ra
N-terminus truncated"
                                                                                                                                                                                                                                     /gene="DKFZp43412411"
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DKFZp434I2411).
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                                                                                                           GCCTCGGAGCTCGTGCACTATGGCTTCCTCCACGAGGACGACCGGATGAAGCTGGCCGCC
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473

720 453 660 413

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480 373 420 353 360 300

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Inferring nonneutral evolution from human-chimp-mouse orthologous
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Pan troglodytes NRBP gene, VIRTUAL
genomic survey sequence
AY408904
AY408904.1 GI:39764872
GSS.
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Direct Submission
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This sequence was made by sequencing genothem based on alignment.
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Science 302 (5652), 1960-1963 (2003)
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1 (bases 1 to 1601)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                       GluArgGluAspGluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArg
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                                                                                          CTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGGAATGAGGTACAGTTCTCTGAG
                                                                                                                                                                 LeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAsp
                                                       ValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCys
                                         TTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="NRBP"
/locus_tag="HCM3379"
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                                                                                                                                                                                                                                                                                                                                                 4.51e-152
1534.50
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    GAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGAC
                  AspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAsp
                                                      VallleGlnMetGlnCysAsnLeuGluArgSerGluAspLysAlaArgTrpHisLeuThr
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	Qy 77 ArgLysAlaPheAlaAlaI	Db 250 CTGGCCATGGATACAGAGG	, ,	Qy 37 TrpGlnLyeArgArgGluc	Db 130 GAGGAAGAAGAAGT	17	US-10-618-941-99 (1-507) x AY408903		P P	ORIGIN Alignment Scores:	/locus_tag="HCM3379"	/db_xref="te gene <1>1608 /gene="NDBBB		Loca	COMMENT This sequence was made by seq them based on alignment.		Ferriera, S., Wang, G., Adams, M.D. and Cargi	AUTHORS Clark, A.G., Glanowsk: Todd.M.A. Tanenhaum	JOURNAL Science 302 (5652), 1 PUBMED 14671302	TITLE Inferring nonneutral evol	Todd, M.A., Ferriera, S	REFERENCE 1 (bases 1 to 1608) AUTHORS Clark, A.G., Glanowsk:	Mammalia; Butheria; I Hominidae; Homo.	ns (human) 19	AY408903.1 G GSS.	7	ens NF	T 7	Db 1503 CAGAGCCGGTTGACTTCTC	Oy 488 ArgMetLysLeuAlaAla1
CHARMACHARMACH TARTATATATATATATATATATATATATATATATATATA	ArgLysAlaPheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeu 96	CTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGGAATGAGGTACAGTTCTCTGAA 309		TrpGlnLyeArgArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPhe 56	GAGGAAGAAGAAGATGAAGATGAGTCTGAGATTTTGGAAGAGTCGCCCTGTGGGCGC 189		903 (1-1608)	Indels: Gaps:	2 Length: 1608 Matches: 305 Conservative: 59 Mismatches: 102		"HCM3379"	axon:9606"	Janism="Homo sapiens"	alifiers	de by sequencing genomic exons and ordering ent.	Direct Submission  AL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	, Zheng,X.H., White,T.J., Sninsky,J.J., 11,M.	i,S., Nielson,R., Thomas,P., Kejariwal,A.,	1960-1963 (2003)	evolution from human-chimp-mouse orthologous	, Civello,D.R., Lu,F., Mng,X.H., White,T.J., Sni	i,S., Nielson,R., Thomas,P., Kejariwal,A.,	Euarchontoglires; Primates; Catarrhini;		871	·	gene, VIRTUAL TRANSCRIPT, partial sequence,		CAGAGCCGGTTGACTTCTCTCCTAGAAGAGACCTTGAACAAGTTC 1547	ArgMetLyeLeuAlaAlaPheLeuGluSerThrPheLeuLyeTyr 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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1 (bases 1 to 2137)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

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HTC; CNSLT_CDNA.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/tissue_type="placenta Cot 25-normalized"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgAlaArgHisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAla
               GTCGTGCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAAG
                                                                                                                                                                                                                                                           GAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAGTGCCGTACTGGCTGAAATC
                                                                                                                                                                                                                                                                            GluAsnValValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaValLeuGluIleGlnThrAsnGlyAspThrArg---ValThrGluGluAlaIleAla
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                                                                                               ThrArgProLeuGlyLeuProArgValLeuAlaProProProGluGluVal------
                                                                                                                                     TTAGATAAATTCCTTGAAGATGTCAGGAATGGGATCTATCCTCTGACAGCCTTT-----
                                                                                                                                                                                                                       ProArg---ProArgArgProProLeuGlnTrpArgTyrSerGluValSerPheMetGlu
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                                 -GlnLysAlaLysThrProThrProGluProPheAspSerGluThrArgLys
                                                                           GGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACCT 1368
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemannedkfz-heidelberg.de;
sequenced by Medigenomix (Martinaried/Germany) within the cDNA
sequencing consortium of the German Genome Project.
This clone (DKFZp564D1878) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp564D1878
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp564D1878
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AL136682.1
HTC.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The German cDNA Consortium
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Mewes,H.W., Weil,B., Amid,C.,
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1 (bases 1 to 2158)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
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/db_xref="UniProt/Trembl:Q9UHY1"
/tranalation="MABGE8G(TVLSSGSDFK/ESSSSAPGL/TSVSPPVTSTTSAASPE
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FLKKYKKNHKTWNEKAWKRWCTQILSALSYLHSCDPFITHGNLTCDTIFIQHNGLIKI
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X1-zblüe; sites NotI + SalI"
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                                                                                                                                                               /gene="DKFZp564D1878"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                        clone="DKFZp564D1878"
                                                                                                                                                                                                                                       'note="nuclear receptor binding protein"
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_xref="taxon:9606"
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Osanger,A., Fobo,G., Han,M. and
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NGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLK LLAAHCIVGHQHMIPENALEEITKNNDTSAVLAEIPAGPGREPVQTLYSQSPALELDK FLEDVENGIYPLTAFGLPRPQQPEEVTSPVVPPSVKTPTPEPAEVETRKVVLMQCN IESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEADQSRLT SLLEETLNKFNFARNSTLNSAAVTVSS"

Similarity: ArgAlaArgHisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAla GCAGTGCTGGAGATTCAGGGCAATGGAGAGTCCTCATATGTGCCACAGGAAGCCCATCAGC AlaValLeuGluIleGlnThrAsnGlyAspThrArg---ValThrGluGluAlaIleAla GTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGGCATGTGTGCACTGGAGATG ValAlaAsp---GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet GTGAAGACTTGTCGAGAAGAGCAGAAGAATCTACACTTCTTTGCACCAGAGTATGGAGAA IleArgAlaGluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGlu ThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHis ATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCCATCATCCATGGGAACCTG IleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeu LysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln AlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys TTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGGCTGACATTAAAGAGAACAAG ValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCys CTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGAA LeuAlaMetAspThrGluGluValGluValValTrpAsnGluLeuHisPheGlyAsp 76 TGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATAC GAGGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTTGGAAGAGTCGCCCTGTGGGCGC GluArgGluAspGluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArg 36 ArgIlePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerPro **AAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACAA** GCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAAG CGCAAGAACTACAAGCTGCAGGAGGAAAAGGTTCGTGCTGTTTTGATAATCTGATTCAA ArgLysAlaPheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeu TrpGlnLysArgArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPhe ACCTGTGACACCATCTTCATCCAGCACAACGGACTCATCAAGATTGGCTCTGTG-----(1-507) x HSM801650 7.15e-152 1534.50 73.54% 61.62% 57.47% (1-2158)Length: Matches: Conservative: Mismatches: Indels: Gaps: ----GCTCCTGACACTATCAACAATCAT 2158 305 59 102 29

516 116 456 96 56

276

336

396

1014 294 274

894 255 834 236 774 216 196 696 176 636 156 576 136

750

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RESULT 10
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SOURCE
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ACCESSION
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TITLE
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Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ), Email s.wiemann@dkfz-heidelberg.de;
Reguenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp459G2032) is available at the RZPD Deutsches
Ressourcenzentrum fluer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp459G2032
Further information about the clone and the sequencing project is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pongo pygmaeus mRNA; cDi
CR858669
CR858669.1 GI:55728271
                                                                                                                                                                                                                                                                                      Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluArgGluAspGluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArg
                                                                                                                                            GCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAAG
                                                                                                                                                                 AlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys
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                                                                                  LysThrLysLysAsnH1sLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln
                                                                                                                                                                                                                              TTGGAGCATCTTAACATTGTTAAGTTTCACAAATACTGGGCTGACATTAAAGAGAACAAG
                                                                                                                                                                                                                                                                                                              CGCAAGAACTACAAGCTGCAGGAGGAAAAAGGTTCGTGCTGTGTTTGATAATCTGATTCAG
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/clone_lib="459 (synonym: pcor1). Vector pSport1_Sfi;
DH10B; sites SfilA + SfilB"
/dev_stage="adult"
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/mol_type="mRNA"
/db_xref="taxon:9600"
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1534.50
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ATCCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCCATCATCCATGGGAACCTG

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RESULT 11
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Submitted (20-JUL-2004) Genoscope
BP 191 91006 EVRY cedex - FRANCE (
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 2086)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope
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Hominidae; Homo.
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CR591118
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HTC; CNSLT_CDNA.
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Homo sapiens
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LysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln
                                                                  AlaArgVall1ePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys
                                                                                                                  TTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAAG
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/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK009YM06"
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                                                                                                                         AspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hara, A., Hashizume, W., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, Pax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length CDNAs
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 420, 563-573 6 (bases 1 to 2181)
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Research annotation

Carninci, P.

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Yokohama

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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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uThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHi
                                  GATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCTCCCATCATCCATGGGAACCT
                                                                                                                                               sLysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGl
                                                                                                                                                                                                                                  sAlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLy
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                                                              nIleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLe
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/dev_stage="8 days embryo"
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                                                                                                                                                                     spArgMetLysLeuAlaAlaPheLeuGluSerThrPheLeuLysTyrArgGlyThrGln 506
                                                                                                                                                                                                             atgagagcatcccggacttcgcagctgagctggtgcagctgggcttcattagtgaggctg
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      uValAlaAsp---GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMe

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      AGTCACAAACGTGACAACAGCAGTGGACATCTACTCCTTTGGCATGTGTGCACTGGAGAT

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Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
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http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9017 Contact:
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RZPD; RZPDp9017B1314.
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                                            AlaLeuGluMetAlaValLeuGluIleGlnThrAsnGlyAspThrArgValThrGluGlu
                                                                                                   ProGluTyrGlyGluValAlaAspGlyThrAlaValAspIlePheSerPheGlyMetCys 251
                                                                                    CCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATCTTCTCCTTTTGGGATGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RZPDp9017B1314"
/tissue_type="T-Lymphocytes"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="maxon:9606"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
/clone_lib="RZPD no.9017"
/note="Vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
/mol_type="mRNA"
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Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0BAG070ZB10_CS06698_2.
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                                                                                                                                                                                                         Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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               AsnLeuGluArgSerGluAspLysAlaArgTrpHisLeuThrLeuLeuLeuValLeuGlu
                                                                            LysThrProThrProGluProPheAspSerGluThrArgLysValIleGlnMetGlnCys
                                                                                                                                                ThrArgProLeuGlyLeuProArgValLeuAlaProProProGluGluValGlnLysAla
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                                                                                                                             ACTCGACCCCTGNGGCTGCCCGTGTGCTGGCCCCACCCCGGAGGAGGTCCAAAAAGGCC
                                                                                                                                                                                             CTGGACAAATTCCTGGAGGATGTCAGGAATGGAATCTACCCACTGATGAACTTTGCAGCC
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODN002YIO9"
/tissue_type="ADULT BRAIN"
/dev_stäge="adult"
/dev_stäge="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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KEYWORDS
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia D
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIB00 row: n column: 13
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (bases 1 to 825)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectio
Unpublished (1999)
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Location/Qualifiers
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                                                                                                                                                                                                                                          /tissue_type="tumor, gross tissue"
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam3"
/clone_lib="NCI_CGAP_Mam3"
/note="organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:5315916"
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/strain="129,C57BL/6J,FVB/N"
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Search completed: January 14, 2006, 00:46:08 Job time: 4643 secs

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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

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Compugen Ltd.
                Sequence 10, Appl sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 10, Appl Sequence 36, Appl Sequence 35, Appl Sequence 35, Appl Sequence 34, Appl Sequence 34, Appl Sequence 3173, Appl Sequence 40, Appl Sequence 46950, A Sequence 60, Appl Sequence 60, Appl Sequence 44, Appl Sequence 44, Appl Sequence 44, Appl Sequence 44, Appl Sequence 48, Appl Sequence 54, Appl Sequence 5
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45	44	43	42	41	40	39	38	37	36	35	34	S S	32	31	30	29	0
359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	
13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	
2048	2032	2032	2004	2004	1999	1999	1971	1971	1939	1939	1911	1911	982	982	954	954	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
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US-09-854-856-62	US-10-010-720-42	US-09-854-856-42	US-10-010-720-58	US-09-854-856-58	US-10-010-720-16	US-09-854-856-16	US-10-010-720-32	US-09-854-856-32	US-10-010-720-48	US-09-854-856-48	US-10-010-720-64	US-09-854-856-64	US-10-010-720-6	US-09-854-856-6	US-10-010-720-22	US-09-854-856-22	40 040 000
Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Contraction						
62,	42,	42,	58,	58,	16,	16,	32,	32,	48,	48,	64,	64,	0	6	22,	22,	000
Appl	App1	Appl	App1	Appl	Appl	Appl	Appli	Appli	Appl	App1	23.2						

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 62

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 326

TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(326)

OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09345473E
PATENT NO. 6558903
GENERRAL INFORMATION:
APPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558903el Kinases and Uses
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
                   59.2%;
Score 1580; DB 2;
Pred. No. 1.2e-145;
0; Mismatches 2;
                                       Length
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   Indels
                                       326;
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 Gaps
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120

71 60

180 131

305

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APPLICANT: Hodge, Martin R.

FILE REFERENCE: 35800/234862

CURRENT APPLICATION NUMBER: US/09/862,027

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: US 09/345,473

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 82

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10
                                           GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     RESULT 3
US-08-933-750C-20
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US-09-862-027-10
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Best Local S
Matches 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(326)
OTHER INFORMATION: Xaa = Any Amino Acid
-09-862-027-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
 STREET:
                                ADDRESSEE:
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Similarity 97.4%;
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                   E: Incyte Pharmaceuticals,
3174 Porter Drive
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Pred. No. 1.2e-145;
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US-08-933-750C-20
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Best Local Similarity 61.6%;
Matches 305; Conservative 5
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SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNMER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FRANCEQ for Windows Ver
SOFTWARE: FRANCEQ for Windows Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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 QSRLTSLLEETLNKF
                                RMKLAAFLESTFLKY 502
                                                                 VVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEAD
                                                                                 LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEV-----QKAKTPTPEPFDSETRK
                                                                                                                                                                                                                                                                  AVLEIQGNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFE
                                                                                                                                                                                                                                                                                                   AVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE
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                                                                                                                                  LDKFLEDVRNGIYPLTAF-----GLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRK
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518
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Pred. No. 7e-141;
9; Mismatches 10
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US-09-234-613-20
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GENERAL INFORMATION:
APPLICANT: Lal, Pro
APPLICANT: Hillman,
APPLICANT: Bandman,
                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 305
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                                                                                                                                                                                                                                                                                                                   -09-234-613-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 9F-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUTO
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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ADDRESSEE: Incyte Ph
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CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                               CLONE: 864683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/234,613
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                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                      164
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                                                                                                                                                                                                                                               h 57.5%; Score 1534.5; DB 2; Similarity 61.6%; Pred. No. 7e-141; 05; Conservative 59; Mismatches 102;
RIFSNALRPFTALPDDLRSPIRAEREELRNLHFFPPEYGEVAD-GTAVDIFSFGMCALEM
                                                                       KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH 196
                                                  KTKKOHKTMNEKAWKKWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSV--
                                                                                                                                      RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK 136
                                                                                                                                                                                                                                                                                                                                                                                                                              535 amino acids
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Bandman, Olga
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 500-10-30
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 562
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7299
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                      197
                                                                                                                                                                                                               191
                                                                                                                                                                                                                                                                                         131 RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 QSRLTSLLEETLNKF
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                                                                                                                                                                                                                                                                                                                                                                           71 EEEESSEDESEILEESPCGRWQKKREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSE 130
                                                                                                                                                                                                                                                                                                                                                                                                 17 EREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGD
                                                                                                                                                                                                                                 AVLEIOTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE
                                                                                                                                                                RIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVAD-GTAVDIFSFGMCALEM
VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFME
                                         AVLEIQGNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFE
                                                                                                                           -----APDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEM
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Pred. No. 7.5e-141;
9; Mismatches 102;
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                                                              Query Match
Best Local S
Matches 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09023942A Patent No. 6479274
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PO5101/97
PRILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION UMBER: PP0422/97
PRIOR APPLICATION DATA:
PRILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                             TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John TITLE OF INVENTION: NOVEL MOLECULES NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                            TOPOLOGY: 11
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: Interprinting DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGICILO, FRANK S
REGISTRATION NUMBER: 31,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/023,942A FILING DATE: 13-FEB-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                    TYPE: amino acids
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                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFLHEDD
                         EREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGD
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                                                                Conservative
                                                                                                                                          linear
                                                                                                                             protein
                                                                         56.5%;
                                                                                                                                                                                                                                                                                                                       International
                                                              60;
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                                                             Score 1508.5; DB 2;
Pred. No. 2.4e-138;
0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version
                                                                                                                                                                                                                                                                                                                     PCT Application
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                                                              Indels
                                                                                      Length
                                                                                      535,
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                                                             Gaps
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             103
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      RESULT 8
US-09-862-027-36
US-09-862-027-36
Sequence 36, Application US/09862027
Patent No. 6858418
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GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                        LENGTH:
TYPE: PR
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US-09-345-473E-36
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US-09-345-473E-36
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SEQ ID NO 36
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6558903
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558903el Kinases &
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: C. elegans
                                                                                                                       79 AFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKT 138
                                                                                                                                                                                 23 DSDADGAEETLEESPOKRWSKRREOVKORDVPGIDVAYLAMDNETGNEVVWNEVQFSERK
                                                                                                                                                                                                                         19 EDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGDRK
                                                                                                                                                                                                                                                                                               Similarity
RKAGSSLSIKAWKKWTTQILSALNYLHSSDPPIIHGNLTCNTVFIQQNGLIKIG 196
                            KKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEV------QKAKTPTPEPFDSETRK
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                                                                                      NFRAQEEKINAVFONLTQLVHTNLVKFHKYWTDSKSEKPRIIFITEYMSSGSMSAFLQRT
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                                                                                                                                                                                                                                                                       Score 543; DB 2;
Pred. No. 1.2e-44;
1; Mismatches 45
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; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: NO. 6658418el Kinases and Us;
; FILE REFERENCE: 35800/234662
; CURRENT APPLICATION NUMBER: US/09/862,027
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 36
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; ORGANISM: C. (
US-09-345-473E-35
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US-09-345-473E-35
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SOFTWARE: FASTSEQ for
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                        Matches 116;
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6558903
GENERAL INFORMATION:
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Best Local (
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TITLE OF INVENTION: No. 6558903el Kinabes :
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
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TYPE: PRT
ORGANISM: C.
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      LPGQSSQPSGTTTNTNGPSSIGKSASPEAVDKKIGEVTSTESTSKVEVEVNGANVTIGSS
                                       LPRVLAPP----
                                                                  RNGIYPLTAFAPLAHQPSTTLRAYSNTNPSTLITTDISAPSSTHPSANSTITAETSVNTS
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GENERAL INFORMATION:
APPLICANT: HOdge, Martin
TITLE OF INVENTION: No. 6558903el Kinases &
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
                                                                                              Sequence 34, Application US/09345473E Patent No. 6558903
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RESULT 11
US-09-345-473E-34
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US-09-862-027-35
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CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 116;
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Best Local Similarity
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TITLE OF INVENTION: No. 6858418el Kinases
FILE REFERENCE: 35800/234862
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                                                                                                               LTYDLLPTDSAQDLASELVHYGFLHEDD 487
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Pred. No. 8.9e-32;
7; Mismatches 92;
                                                                                                                                                                                                                                                                      PEEVQK---
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6558903el Kinases and

Uses

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Sequence 34, Application US/09862027

Patent No. 6858418

GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. 6858418el Kinases and FILE REFERENCE: 35800/234862

CURRENT APPLICATION NUMBER: US/09/862,027

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: US 09/345,473

PRIOR APPLICATION NUMBER: US 09/345,473

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 82

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 34

LENGTH: 516

TYPE: PRT
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US-09-862-027-34
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US-09-862-027-34
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SOFTWARE: FAStSEQ for Windows Version
SEQ ID NO 34
LENGTH: 516
                                                                                              Matches
                                                                                                                   Query Match
Best Local :
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Best Local Similarity
Matches 119; Conserv
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                                        REDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGDR
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                       RODENNSEEEFVEIDFTGRYGRYKEVLGKG---AFKEVYRAFDQLEGIEVAWNQVKLDDK
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                                                                                              13.9%;
llarity 25.3%;
Conservative 88
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                                                                                              Score 372; DB 2; Length 516;
Pred. No. 1.9e-27;
8; Mismatches 176; Indels
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; Patent No. 6558903
; GENERAL INFORMATION:
   APPLICANT: Hodge, Martin
   TITLE OF INVENTION: No. 6558903el Kinases and Use
   FILE REFERENCE: 35800/183781
; CURRENT APPLICATION UMBER: US/09/345,473E
; CURRENT FILING DATE: 1999.06-30
; NUMBER OF SEQ ID NOS: 62
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US-09-345-473E-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.8%;
Best Local Similarity 25.0%;
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LCCLARDPARRPSAHSLLFH--RVLFEVHS-LKLLAAHCFIQHQYLMPENV----VEEKT 342
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                                                                                                                                   RDLKCDNIFITGTTGSVKIGDLGLATLKNK-----
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US-09-862-027-40
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Patent No. 6858418
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. 6858418el Kinases and Uses Thereof
FILE REFRENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US/09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
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Best Local Similarity
Matches 128; Conserv
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                                                                                                                                                     KAMDLHAVLAELPRPRRPPLQWRYSEVSFMELD--KFLEDVRNGIYPLMNFAATRPLGLP
                                                                                                                                                                                                                                                                                             EYGEVADGTAVDIFSFGMCALEMAVLEI---QTNGDTRVTEEAIARARHSLSDPNMREFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACA 117 : | | | | | | :::: |
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                                                  ----DSPDEVVQQMIEQQHIPDEDTRMITKL----IKDKV-
                                                                                                                    RDADLNDLNVEIQMQLRVYDEKKRKQYRFKENEGLQFAFDIEN---
                                                                                                                                                                                                                                                                                                                                RDLKCDNIFITGTTGSVKIGDLGLATLKNK-----SFAKSVIGTPEFMAP
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                                                                                 RVLAPPPEEVQKAKTPTPEPFDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQL
                                                                                                                                                                                         -- CFSRIPAQYPBIREIIDRCIRVRREERSTVKQL----LVDDFFTPEDLIGIRVEIKN
                                                                                                                                                                                                                                                              EMYEEMYDESVDVYAFGMCLLEMVTGEYPYSECMNPATIYRKVISGVKPE------
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Pred. No. 2.2e-26;
8; Mismatches 188;
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Search completed: January 12, Job time: 26 secs
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US-09-270-767-31733
                                                                                                                                                                                                                                                                 ; ORGANISM: Drosophila melanogaster US-09-270-767-31733
                                                                                                                                                                                                                                                                                                                            APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31733
                                                                                                                                                                                                                   Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31733, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                     Matches
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TYPE: PRT
                                                                                  178 SDTIFIQHNGLIKIGSVWHRIFSNALRPFTALPDDLRSPIRAEREELRNLHFF-PPEY 234
                                                                                                                                                                 118 RVIFITEYVSSGSLKOFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLT 177
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                                                                63 CDSIFIQHNGLVKIGSV--
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                                                                                                                                 RVVFITEYMSSGSLKQFLKRTKRNAKRLPLESWRRWCTQILSALSYLHSCSPPIIHGNLT
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61.0%;
               2006,
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                 11:23:01
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                                                                --VPDAVHYSVRRGRERERERERGAHYFQAPEY 110
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                                                                                                                                                                                                                                   Length 110;
                                                                                                                                                                                                  11;
                                                                                                                                                                                                Gaps
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US0_NEW_COMB.pep:*
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2670
1 MAAPEPAPRAREREREBED.....RMKLAAFLESTFLKYRGTQA
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US-11-214-063A-1714
US-60-752-355-3150
US-60-752-355-31780
US-60-752-355-31780
US-60-752-355-1875
US-60-752-355-1875
US-60-752-355-24004
US-60-752-355-24004
US-60-752-355-21991
US-60-752-355-21991
US-60-752-355-21873
US-60-752-355-3183
US-60-752-355-3183
US-60-752-355-46137
US-60-752-355-46137
US-60-752-355-3513141
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Compugen Ltd.
Sequence 1714, Ap
Sequence 38255, Ap
Sequence 5150, Ap
Sequence 13134, A
Sequence 11780, A
Sequence 11780, A
Sequence 1875, Ap
Sequence 35913, A
Sequence 35913, A
Sequence 30838, A
Sequence 10912, A
Sequence 31813, A
Sequence 18183, A
Sequence 18183, A
Sequence 18183, A
Sequence 18183, A
Sequence 1874, Ap
Sequence 31341, A
Sequence 31341, A
Sequence 15627, A
Sequence 15747, A
Sequence 15747, A
Sequence 15747, A
Sequence 15747, A
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RESULT 1 US-11-214-063A-1714

ALIGNMENTS

179 6.7 1208 7 US-61-311-940-783 179 6.7 1208 WS-60-752-355-3110 178 6.7 915 WS-60-752-355-34116 176 6.6 589 WS-60-752-355-34116 176 6.6 589 WS-60-752-355-21013 175 6.6 1038 7 US-11-311-940-5630 177 6.5 671 WS-60-752-355-33163 178 6.5 1533 WS-60-752-355-43360 179 6.5 1533 WS-60-752-355-43360 179 6.5 1230 WS-60-752-355-47449 170 6.4 1367 WS-60-752-355-2747 171 6.4 661 WS-60-752-355-2747 171 6.4 661 WS-60-752-355-29404 171 6.4 661 WS-60-752-355-29404 171 6.4 662 WS-60-752-355-29404 170 6.4 1230 WS-60-752-355-29404 171 6.4 661 WS-60-752-355-29404 171 6.4 661 WS-60-752-355-29404 171 6.4 662 WS-60-752-355-350-718	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27
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	1230	602	666	661	520	1955	1367	1230	954	612	1533	671	1038	777	589	486	915	1208	1208
US-11-311-940-783 US-60-752-355-38028 US-60-752-355-34116 US-60-752-355-24018 US-60-752-355-21013 US-11-311-940-5630 US-60-752-355-31969 US-60-752-355-48360 US-60-752-355-48360 US-60-752-355-48360 US-60-752-355-2747 US-60-752-355-2747 US-60-752-355-2748 US-60-752-355-2747 US-60-752-355-2747 US-60-752-355-2747 US-60-752-355-27404 US-60-752-355-29404 US-60-752-355-29404 US-60-752-355-29404 US-60-752-355-29404 US-60-752-355-29404 US-60-752-355-29404	8	œ	8	8	7	æ	œ	æ	œ	œ	œ	œ	7	œ	œ	œ	œ	œ	7
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	9718, Ap	43802, 1	33807, 1	29404, 1	7858, A	36649, 1	•	•	•	48360, A	33969, 1	43173, Ā	5630, Ap	21013, A	-	34116, 1	38028, A	15110, /	783, App

## APPLICANT: SUWA, MAKIKO APPLICANT: ASAI, KIYOSHI APPLICANT: ASAI, KIYOSHI APPLICANT: AKIYAMA, YUTAKA APPLICANT: AKIYAMA, YUTAKA APPLICANT: AKIYAMA, YUTAKA APPLICANT: ABURATANI, HIROYUKI TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS FILE REFERENCE: 084335/166 CURRENT APPLICATION NUMBER: US/11/214,063A CURRENT APPLICATION NUMBER: US/10/292,798 PRIOR APPLICATION NUMBER: US/10/292,798 PRIOR APPLICATION NUMBER: US/10/292,798 PRIOR APPLICATION NUMBER: 10/017,161 PRIOR APPLICATION NUMBER: 10/017,161 PRIOR PILING DATE: 2001-12-18 PRIOR APPLICATION NUMBER: US/10/292,798 PRIOR FILING DATE: 2001-06-18 NUMBER OF SEQ ID NOS: 2070 SOPTWARE: Patentin Ver. 2.1 SEQ ID NO 1714 LENGTH: 752 TYPE: PRT ORGANISM: Homo sapiens US-11-214-063A-1714 ঠ 5 S 밁 뭐 밁 S 밁 Query Match 33.1%; Score 882.5; DB 7; Best Local Similarity 42.2%; Pred. No. 1.3e-75; Matches 201; Conservative 39; Mismatches 67; Sequence 1714, Application US/11214063A GENERAL INFORMATION: 257 VLEIQTNGDTRVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFEVH 137 KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH 196 138 RKNY-----KLQEVVAPL-------TAQCPH------77 RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSBACARVIFITEYVSSGSLKQFLK 136 RIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMA -----SYLHSCOPPIIHGNLTCOTIFIQHNGLIKIGS---Indels 169; Length 752; Gaps 188 156 208

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Sequence 30255, Application US/60752355
GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with end
FILE REFERENCE: 38-21(53720) B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
SOFTWARE: PatentIn version 3.3
SEQ ID NO 38255
LENGTH: 554
TYPE: PRT
ORGANISM: OTYZA SALIVA
US-60-752-355-38255
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Best Local (
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Local Similarity 22.8%;
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VPDPWLEISQLKAP---
                                 LAPPPEEVQKAKTPTPEPFDSETR 426
                                                                                                             RPRRP---PL-QWRYSEVSFMELDKF-----LEDVRNGIYPLMNFAATRPLGLPRV
                                                                                                                                                                                                                                                                   HSLSDPNM-----REFILCCLARDPARRPSAHSLLFHRVLFEV-------
                                                                                                                                                                                                                                                                                                                                             REELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLE---IQTNGDTRVTEEAIARAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - NMPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVL--- VDHPNIV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMOCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFLHE 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQ-
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                                                                                                                                                                                                                               NSKDIPDIPDHLSFEAKNFLKLCLQRDPAARPTAAQLMEHPFVKDLVANRSFRSGMTRDT
                                                                                                                                                                                                                                                                                                           PEVIMNTNGY-----SLSVDIWSLGCTIIEMATARPPWIQYEG-----VAAIFKIG 361
                                                                                                                                                                                                                                                                                                                                                                                   LHGRN--TVHRDIKGANILVDPNGDIKLADFGMAKH-----ISAHTSIKSFKGSPYWMA
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                                                                         LPVSPCSSPLRQYRQSNRSCMPSPPHPAYSAGAANYSPINNALYP-----KRP---SNH
                                                                                                                                                   FPTSFDGKGAMVQTSNRSLSPLRDPDLTMRNLQVPTSAIPSISTRRISAINPSNVRMNMS
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                                                                                                                                                                                         -HSLKLLAAHCFIQHQYLMPENVV----EEKTKAMDLHAVLAELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 199; DB 8;
Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PGSPCSSSRVVSSQWKKGKLLGSGTFGQVYQG
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RESULT 4

US-60-752-355-13134

US-60-752-355-13134

Sequence 13134, Application US/60752355

GENERAL INFORMATION:

APPLICANT: Abad, Mark et al.

TITLE OF INVENTION: Transgenic plants with enl

FILE REFERENCE: 38-21(53720)B

CURRENT APPLICATION NUMBER: US/60/752,355

CURRENT ETLING DATE: 2005-12-21

NUMBER OF SEQ ID NOS: 52803

SOFTWARE: PatentIn version 3.3

SEQ ID NO 13134

LENGTH: 894

TYPE: PRT
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Sequence 5150, Application US/60752355

GENERAL INFORMATION:

APPLICANT: Abad, Mark et al.

TITLE OF INVENTION: Transgenic plants with enl

FILE REFERENCE: 38-21(53720) B

CURRENT APPLICATION NUMBER: US/60/752,355

CURRENT FILING DATE: 2005-12-21

NUMBER OF SEQ ID NOS: 52803
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; NAME/KEY: misc feature
; LOCATION: (726)..(726)
; OTHER INFORMATION: Xaa
US-60-752-355-5150
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                                                       ; ORGANISM: Oryza
US-60-752-355-13134
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SEQ ID NO 5150
LENGTH: 833
Query Match
Best Local Similarity
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NAME/KEY: misc feature
LOCATION: (695)...(695)
OTHER INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452 SAKQLGQEISLLSRLQHPNIVQYY-----GSETVDDKLYIYLBYVSGGSIHKLLQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 SPGSRWKK-----GKLIG-RGTFGHVYVGFNSDSGEMCAMKEVTLFLDDPKS----KE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 SPCGRWQKRREQVNQGNMPGLQSTF----LAMDTEEGVEVVWNE--LHFGDRKAFAAHEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FEVHSLKLLAAHCFIQHQYLMPENVVEE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---IQTNGDTRV----TEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVL
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                                                                         sativa (japonica cultivar-group)
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7.3%;
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Score 196;
Pred. No.
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Pred. No. 4e-10;
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 196; DB 8;
No. 4.5e-10;
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                   Length 894;
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Sequence 31780, Application US/60752355
(GENERAL INFORMATION:
APPLICAUT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with enl
FILE REFERENCE: 38-21(53720)B
(CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
SOFTWARE: Patentin version 3.3
SEQ ID NO 31780
LENGTH: 894
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US-60-752-355-31780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
      313
                                        607
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                                                                                                                                                                                                                                   HKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSN 201
                                                                                                                                                                                                                                                                           SAKQLGQEISLLSRLQHPNIVQYY-----GSETVDDKLYIYLEYVSGGSIHKLLQE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIQTVFEQLVL----VDHPNIVKLHKYWLDTSEACARVIFI-TEYVSSGSLKQFLKKTKKN 141
    FEVHSLKLLAAHCFIQHQYLMPENVVEE 340
                                                                                                                                                         ALRPPTALPODLRSPIRAEREELRNLHFFPPEYGEVADG--TAVDIFSFGMCALEMAVLE 259
                                                                                                                                                                                                 YGQLGEQAIRSYTQQILSGLAYLHAKN--TVHRDIKGANILVDPSGRVKLADFGMAKHIN
                                                                                                                                                                                                                                                                                                                                                      SPGSRWKK-----GKLIG-RGTFGHVYVGFNSDSGEMCAMKEVTLFLDDPKS----KE
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                                        PPWSQYEGIAAMFKIGNSKELPPIPDHLSEPG-KDFIRKCLQRDPSQRPTAMELL----
                                                                                                                    GOOCPESEKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPWSQYEGIAAMFKIGNSKELPPIPDHLSEPG-KDFIRKCLQRDPSQRPTAMELL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALRPPTALPODLRSPIRAEREELRNLHFFPPEYGEVADG--TAVDIFSFGMCALEMAVLE 259
                                                                              ---IQTNGDTRV----TEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVL 312
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                                                                                                                    -SP-----YWMAPEVIKNSNGCNLAVDÍWSLGCTVLEMATSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 196; DB 8;
Pred. No. 4.5e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 894;
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GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with en
FILE REFERENCE: 38-21(53720) B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
SOUTMARE: Patentin version 3.3
SEQ ID NO 11788
LENGTH: 600
TYPE: PRT
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US-60-752-355-1875
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US-60-752-355-11788
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                                                                                                              Sequence 1875, Application US/60752355
GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with
FILE REFERENCE: 38-21(53720)B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
                    NUMBER OF SEQ ID NOS: 52803
SOFTWARE: Patentin version 3.3
SEQ ID NO 1875
LENGTH: 611
TYPE: PRT
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Best Local
ORGANISM: Nicotiana benthamiana
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Local Similarity 23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 SPCGRWQKRREQVNQGNMPGLQSTF----LAMDTEEG------VEVVWNELHFGDRKAF 80
                                                                                                                                                                                                                                                                                                                                                                      FDSETRK 427
                                                                                                                                                                                                                                                                                                                                                                                                              VLESHSNRTSITSLDG--
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                                                                                                                                                                                                                                                                                                                                  SSSPLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                -LOWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEP 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMAVLEIQTNGDTRVTEEAIARARHSLSDPNMRE-----FILCCLARDPARRPSAHS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKH-----INSSASMLSFKGSPYWMAPEVVMVTNGY------SLPVDIWSLGCTII 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKI---GS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNVSKWRK-----GKLLG-RGTFGHVYLGFNSENGQMCAIKEVKVVSDD------
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Pred. No. 2.8e-10;
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RESULT 8

US-60-752-355-42688

Sequence 42688, Application US/60752355

GENERAL INFORMATION:

TITLE OF INVENTION: Transgenic plants with enly FILE REFERENCE: 38-21(53720)B

CURRENT APPLICATION NUMBER: US/60/752,355

CURRENT FILING DATE: 2005-12-21

NUMBER OF SEQ ID NOS: 52803

SOFTWARE: PatentIn version 3.3

LENGTH: 567
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US-60-752-355-42688
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Best Local S
Matches 86
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Best Local Similarity
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164
                                                         104 KLHKYMLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAMKRWCTQILSALSF 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 HKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKI---GSVWHRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 KWKK-----GKLLG-RGTFGHVYLGFNRENGQMCAIKEVRVVSDD------QTSK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 RWQKRREQVNQGNMPGLQSTF----LAMDTEEG-----VEVVWNELHFGDRKAFAAHE
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                                                                                                                                                                                                                                 Similarity
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LHACSPPIIHGNLTSDTIFIQHNGLIKI----GSVWHRIFSNALRPPTALPDDLRSPIRAE
                                                                                          FNSEGGQ-----MCAIKEVKVISDD------SNSKECLRQLHQEIVLLSQLSHPNIV
                                                                                                                     - NMPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVL--- VDHPNIV
                                                                                                                                                       SSPHPLPRP-----
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                           QY--YGSDLSSETLSVYL--EYVSGGSIHKLLQE----YGAFGEAVLRNYTAQILSGLAY
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                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                Score 193.5; DB 8;
Pred. No. 3.9e-10;
2; Mismatches 107;
                                                                                                                                                     -----PGSPCSSSRVVSSQWKKGKLLGSGTFGQVYQG
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US-60-752-355-24004
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Best Local 9
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US-60-752-355-35913
US-60-752-355-35913
Sequence 35913, Application US/60752355
GENERAL INFORMATION:
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SEQ ID NO 35913
LENGTH: 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with
FILE REFERENCE: 38-21(53720)B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
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1415 GHKPQLPSPEQLSEPGRTFLARCLEHDPTKRPSAVELLADPWMVEIRHM 1463
                                                                                                                                                                                                                     1298 --VVHRDIKPENVLLDHNGVIKYVDFGAA-KVIASNGRTIGGMTNSSLRKSVKRDGHNNL 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1135 KIEERRRNLQEEFQSIGRVLDVSDSEYQFLTLLASSFSSVSIRWQK-GACIGRGT---FG 1190
                                                                                                                                                                                                                                                                                                                                                                                  109 WLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 RAREREREDESEDESDILEESPCG----
                                                                                                                                                                                                                                                                                                                                                                                                                                     HSLSDPNM-----REFILCCLARDPARRPSAHSLLFH 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPIIHGNLTSDTIFIQHNGLIK---IGSVWHRIFSNALRPPTALPDDLRSPIRAEREELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNI-----VKLHKY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSKDIPDIPDHLSFEAKNFLKLCLQRDPAARPTAAQLMEH 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEVIMNTNGY-----VAAIFKIG 439
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                                                                                                                                              NLHFFPPEY--GEVADGTA-----VDIFSFGMCALEMAVLE---IQTNGDTRVTEEAIA
                                                   RARHSLSDPNM-----REFILCCLARDPARRPSAHSLLFHRVLFEVHSL 318
                                                                                                            NSMTGTPMYMSPEAITGTSTDRSGVVDIWSLGCCVLEMATGRRPWANLDNEWAIMYHIAA
                                                                                                                                                                                                                                                                                                                            -----DKVYIFMEFCEGGSLAGLL----THGRIEDEMVIQVYALQMLEGLAYLHQSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.2%; Score 193; DB 8; 22.6%; Pred. No. 1.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----RWOKRREQVNQGNMPGLQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enhanced agronomic traits
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RESULT 10
US-60-752-355-24004
US-60-752-355-24004
Sequence 24004, Application US/60752355
GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
FILE REFERENCE: 38-21 (53720) B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
SOFTWARE: Patentin version 3.3
SEQ ID NO 24004
LENGTH: 786
TYPE: PRT
ORGANISM: Zea mays
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471

421 507 416

256

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Sequence 10912, Application US/60752355
; GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
APPLICANT: Abad, Mark et al.
FILE OF INVENTION: Transgenic plants with enhanced agr
FILE REFERENCE: 38-21(33720)8
; CURRENT APPLICATION NUMBER: US/60/752,355
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
; SOFTWARE: PatentIn version 3.3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10912
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Lotus corniculatus var. japonicus
US-60-752-355-10912
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US-60-752-355-10912
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                                                                                                                                                                                               Query Match
Best Local S
Matches 106
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 KLHKYWLDTSEAÇARVIFI-TEYYSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALS
138 TKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIG$VWHR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 QVYMGFNSEGGOMCAIKEVKVISDD------SNSKESLRQLNQEIVLLSQLSHPNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 SSPQPLP-----GKLLGSGTFG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109;
                                                                                                                                                  28 ILEESPC--GRWQKRREQVNQGNMPGLQSTF----LAMDTEEGVEVVWNELH-FGDRKAF
                                                                                                                                                                                                   106;
                                                                            81 AAHEEKIQTVFEQLVLVD---HPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKK
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                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYY-----GSDLCNETLSVYLEYVSGGSTHKLLQE----YGPFGEAVLRNYTAQILSGLA
                                     -TSKECLKQLNQEINLLNQFSHPNIVQY--YGSELGEESLSVYL--EYVSGGSIHKLLQE
                                                                                                                 VLENNTCNLSKWKK-----GKLLG-RGTFGHVYLGFNSENGQMCAIKEVKVFSDDK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SSGLTDPWLEISQVKTQT---FDSPRR 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNMSLPVSPCSSPLRQYRQSNRSCLRSPPHPAYSAGAANYNPINNALYP-----TRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AELPRPRRP---PL-QWRYSEVSFMELDKF-----LEDVRNGIYPLMNFAATRPLG 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSTDGKNSRVKIETSSYRSLSP---LRDPDILGRNLPGPTSPIPSTSSRRIAALNTSNVR
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24.9%;
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                                                                                                                                                                                         ; Score 190.5; DB 8; ; Pred. No. 8.8e-10; 57; Mismatches 162;
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                                                                                                                                                                                             Indels 101;
                                                                                                                                                                                                                                  Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agronomic
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 30838
LENGTH: 555
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-60-752-355-30838
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US-60-752-355-30838
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GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with
FILE REFERENCE: 38-21(53720)B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
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                                                                                                                                                                        211 LITKIHKLIMDPIPAMYSGSFRGLIKSMLRKNPELRPSANELL
                                                                                                                                                                                                           272 AIARARHSLSDP------NMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAH 324
                                                                                                                                                                                                                                                   165 GTPS----YMCPELLADIPYGSKSDIWSLGCCMYEMAAHKPPFKASDVQT------
                                                                                                                                                                                                                                                                                        219 AEREELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMA-----VLEIQTNGDTRVTEE
                                                                                                                                                                                                                                                                                                                                                                      159 SALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555 SSPLRQ 560
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                                                                                                                                                                                                                                                                                                                                                                                                             60 NPFVVEYKDSWVE--KGC-YVCIVIGYCQGGDMTDTIKRACGVH--FPEEKLCQWLVQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 HPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 EQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHF---GDRKAFAAHEEKIQTVFEQLVLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
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                                                     NGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPFDSETRKVIQMQCNLERSE 439
                                                                                                                           CFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRP---PLQWRYSEVSFMELDKFLEDVR
                                                                                                                                                                                                                                                                                                                                 MALDYLH--SNHILHRDVKCSNIFLTKEQDIRLGD----FGLA---KILTSDDLTSSVV
                  RS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQIGKGS----FGSALLVRHKQERKKYVLKKIRLARQSDRARRSAHQE-----MELISTVR 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                --SFSNDRRLN-PSVSDTEAGSVSSSGKASPTPM-FNGRKVSEVTVGVVREE
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23.3%; Pred. No. 1.8e-09;
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342

382

253

271 164

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158

114

86

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Sequence 51629, Application US/60752355
GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with en.
FILE REFERENCE: 38-21(53720)B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
SOFTWARE: PatentIn version 3.3
SEQ ID NO 51629
LENGTH: 884
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US-60-751-420-3790
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US-60-752-355-51629
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US-60-751-420-3790
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Matches
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SOFTWARE: Patentin version 3.3
SEQ ID NO 3790
LENGTH: 544
TYPE: PRT
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APPLICANT:
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APPLICANT: Van Eerdewegh, Paul
APPLICANT: Little, Randall David
APPLICANT: Keith, Tim
APPLICANT: Keith, Tim
TITLE OF INVENTION: Genemap of the human genes associated with Crohn's
FILE REFERENCE, GENI-O11/00US
CURRENT APPLICATION NUMBER: US/60/751,420
CURRENT FILING DATE: 2005-12-19
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 7.0%; Score 186; DB 8; Similarity 24.3%; Pred. No. 1.9e-09; 81; Conservative 57; Mismatches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIJHGNLTSDT 180
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Croteau, Pascal
Allard, Rene
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Paquin, Bruno
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APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with en
FILE REFERENCE: 38-21(53720)B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
SOFTWARE: Patentin version 3.3
SEQ ID NO 18183
LENGTH: 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Arabidopsis thaliana US-60-752-355-18183
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US-60-752-355-18183
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Best Local Similarity
Matches 84; Conserv
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                                                                                                                                                                                                                                                                             395 SPGSRWKK-----GRLLGMGSFGHVYLGFNSESGEMCAMKEVTLCSDDPKS----RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 SPGSRWKK-----GRLLGMGSFGHVYLGFNSESGEMCAMKEVTLCSDDPKS----RES
                                           203 LRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADGT--AVDIFSFGMCALEMAVLE-
                                                                                                                                                                                                                             87 IQTVFEQLVLVD---HPNIVKLHKYWLDTSEACARVIFI-TEYVSSGSLKQFLKKTKKNH 142
                                                                                                                                                                                                                                                                                                                         32 SPCGRWQKRREQVNQGNMPGLQS---TFLAMDTEEGVEVVWNE--LHFGDRKAFAAHEEK 86
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QSGPLSFKG---
                                                                                                                                    KAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNA
                                                                                                                                                                                  AQQLGQEISVLSRLRHQNIVQYY-----GSETVDDKLYIYLEYVSGGSIYKLLQE----Y
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                                                                                      GQFGENAIRNYTQQILSGLAYLHAKN--TVHRDIKGANILVDPHGRVKVADFGMAKHITA
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Pred. No. 4e-09;
0; Mismatches 116
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  ----YWMAPEVIKNSNGSNLAVDIWSLGCTVLEMATTKP
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Search c Job time	DЪ	Ş	₽	Ş
Search completed: January 12, 2006, 11:30:50 Job time : 50 Becs	652DHAFVRNVMPMERPIVSGEPAEAMNV 677	310 RVLFEVHSLKLLAAHCFIQHQYLMPENVVE-EKTKAMDL 347	599 PWSQYEGVPAMPKIGNSKELPDIPDHLSEEGKDFVRKCLQRNPANRPTAAQLL 651	260IQTNGDTRVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFH 309

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Result
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RESULT 2
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Hypothetical protein H37N21.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004
C;Accession: T23136; T23575
R;McMurray, A.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z19694

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A;Accession: T23136
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-231 <WIL>
A;Residues: 1-231 <WIL>
A;Residues: 1-231 <WIL>
A;Residues: 1-231 <WIL>
A;Cross-references: UNIPROT:045668; UNIPARC:UPI0000076BE3; EMBL:AL008986; PIDN:CAA15621.
A;Cross-references: UNIPROT: D45668; UNIPARC:UPI0000076BE3; EMBL:AL008986; PIDN:CAA15621.
A;Cross-reference clone H37N21
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19762
A;Accession: T23575
A;Accession: T23575
A;Accession: T23575
A;Accession: T23575
A;Cross-references: UNIPARC:UPI0000076BE3; EMBL:Z75545; PIDN:CAA99888.1; GSPDB:GN00019;
A;Cross-references: UNIPARC:UPI0000076BE3; EMBL:Z75545; PIDN:CAA99888.1; GSPDB:GN00019;
A;Experimental source: clone K10D3
C;Genetics:
A;Gene: CESP:H37N21.1
A;Map position: 1
A;Introns: 31/3; 68/1; 122/3; 152/3; 171/3
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A;Molecule type: DNA
A;Residues: 1-461 <WIL-
A;Cross-references: UNIPROT:Q21419; UNIPARC:UPI000007CFE6; EMBL:
A;Experimental source: clone K10D3
C;Geneeics:
A;Geneeics:
A;Genee: CESP:K10D3.5
A;Map position: 1
A;Introns: 12/1; 40/1; 124/3; 157/3; 212/3; 345/2; 386/3; 421/2
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A;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23574
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19762
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                                                                                          PDDLRSPIRAEREELRNLHFFPPEYGEVADGT-AVDIFSFGMCALEMAV---LEIQTNGD
                                   HCFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRPPLOWRYSEVSF--MELDKFLEDV
                                                                                                                                            PDAINHHVKTCRENMRYMHYIAPEYENNTELTSAADIYSFGICSLEIAVIGGLSGCQNGS
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HAIVDSKKY--EDVSESAFRIKD-NETIAATSKLR----EMAYCQVAAFQVDLEKFLDDV
                                                                      SEGPVTEDVIEKAIRSLEDPMQQDFIRQCLRKDPAERPSARELLFHQILFEVHSLKLLSA
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                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                               15.6%;
                                                                                                                                                                                                              ; Score 415.5; DB 2; ; Pred. No. 6.5e-20; 57; Mismatches 92;
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Pred. No. 1.1e-28;
1); Mismatches 45
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                                                                                                                                                                                                              Indels 123;
                                                                                                                                                                                                                                                 Length 461;
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A;Reference number: 215793
A;Accession: T06716
A;Molecule type: DNA
A;Residues: 1-516 <QUE>
A;Cross-references: UNIPROT:Q9STK6; UNIPARC:UPI00000A845D;
A;Experimental source: cultivar Columbia; BAC clone T29H11
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T29H11.220 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #text_change 05-Oct-2004 C;Date: 23-Apr-1999 #text_change 05-Oct-2004 C;Accession: T06716 R;Quetier, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolice submitted to the Protein Sequence Database, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: ATSP:T29H11.220
A;Map position: 3
A;Introns: 23/3; 36/2; 112/2; 187/1; 239/3; 295/1; 338/1
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                                                                                                                                 RYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPFDSE
                                                                                                                                                                                                                                                                                                             ALEMAVLEIQTNGDT-----RVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAH
                                                                                                                                                                                                                                                                                                                                                                                                -SVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADGTAVDIFSFGMC
                                                                                                                                                                                                                     SLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRPPLQW
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                                         TRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPT----
                                                                                     --SEVGLLTVEGQRKDL-NTIFLKLRITDSK-------GQIRNIHFPFNIETDTS
                                                                                                                                                                             ELLDDPFL
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25.3%; Pred. No. 5.4e-17;
ative 88; Mismatches 176;
                                                                                                                                                                             --KCYKEN----TENVSSHKENGYNGNGIVDKLSD
                                                                                                                                                                                                                                                                                                                                                           ---ARSAHSVIGTPEFMAPELYEEDYNVLVDIYAFGMC
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C;Accession: T02951
R;Kim, C:Y:; Cheon, S:Y:; Cho, M.J.
submitted to the EMBL Data Library, July 1998
A;Description: Identification and characterization
A;Reference number: Z14788
                                                                        probable mitogen activated protein kinase ("Species: Oryza sativa (rice) ("Date: 24-Mar-1999 #sequence_revision 24-C;Accession: T02951 R;Kim, C.Y.; Cheon, S.Y.; Cho, M.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data A, Reference number: Z19204 A, Accession: T19964
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T19964
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              Reference number: Z14788; Accession: T02951
Status: preliminary; translated
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;Introns: 15/3; 42/1;
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;Experimental source: clone C46C2
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                                                                                                                                                                                                                  DHRLLEIKRAKEEEERIREEAEIKEELRLRAEA
                                                                                                                                                                                                                                                                                                                                                                        KAMDLHAVLAELPRPRRPPLOWRYSEVSFMELD--KFLEDVRNGIYPLMNFAATRPLGLP
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                                                                                                                                                                                                                                                 TYDLLPTDSAQDLASELVHYGFLHEDDRMKLAA
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                                                                                                                                                                                                                                                                                                                                           RDADLNDLNVEIQMQLRVYDEKKRKQYRFKENEGLQFAFDIEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMYEEMYDESVDVYAFGMCLLEMVTGEYPYSECMNPATIYRKVISGVKPE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYGEVADGTAVDIFSFGMCALEMAVLEI----QTNGDTRVTEEAIARARHSLSDPNMREFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R----VIFITEYVSSGSLKQFLKKTKK-NHKAMNARAWKRWCTQILSALSFLHACSPPIH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAREREREDES-----EDESDI----LEESPCGRWQKRREQVNQGNMPGLQSTFL
                                                                                                                                                                                                                                                                              ----DSPDEVVQQMIEQQHIPDEDTRMITKL-----IKDKV---
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ilarity 25.0%;
Conservative 8
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from
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Pred. No. 4.7e-16;
B; Mismatches 188;
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                                                                                                     #text_change
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R; Delseny, M.; Berger, ...
submitted to the Protein St
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N;Alternate names: protein T18N14.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000
                                                                 A; Map position: 3
A; Introns: 24/3;
A; Note: T18N14.10
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A;Residues: 1-677 <KIM>
A;Residues: 1-677 <KIM>
A;Cross-references: UNIPROT:O81637; UNIPARC:UPI00000A443B; EMBL:AF080436; NID:g3450841;
A;Experimental source: cultivar Millyang 117
C;Genetics:
A;Gene: MEK1
                                                                                                                                  A;Cross-references: UNIPROT:Q9SCU5; UNIPARC:UPI000009F4A7; A;Experimental source: cultivar Columbia; BAC clone T18N14
                                                                                                                                                                    A; Molecule type:
A; Residues: 1-547
                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                     A; Accession: T46059
 Best Loc
Matches
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                                                                                                                    Genetics:
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3; 113/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BEKIQTVFEQLVL---VDHPNIVKLHKYWLDTSBACARVIFITEYVSSGSLKQFLKKTKK
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                                                                                                                                                                                                                                                  Berger, C.; Cooke,
he Protein Sequence
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   Conservative
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             12.3%;
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 79;
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Score 327.5; DB 2;
Pred. No. 4.8e-14;
9; Mismatches 176;
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Pred. No. 2.3e-15;
1; Mismatches 166
                                                                                                                                                                                                                                                  R.; Grellet, F.; Laudie,
Database, December 1999
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submitted to the EMBL Data Library, May 1999
A; Description: Analysis of Arabidopsis thaliana gene A; Accession: T51099
A; Status: prairies
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Best Local Similarity
Matches 130; Conserv
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Residues: 1-549 <COO>
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                                                                      SVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLH-----FFPPEYGEVADGTAVDI
                                                                                                                                            FLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQ-HNGLIKIG
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                         GLAAILRGS----QNAHSVIGTPEFMAPELYEEDYNELVDI
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R;Ruiz-Perez, V.L.; Murillo, F.J.; Torres-Martinez, S.
Curr. Genet. 28, 309-316, 1995
A;Title: PkpA, a novel Phycomyces blakesleeanus serine/threonine prot
A;Reference number: S59578; MUID:96120859; PMID:8590476
A;Accession: S59578
A;Molecule type: DNA
A;Residues: 1-9;39-346 <RUW>
A;Cross-references: UNIPARC:UPI0000172622; UNIPARC:UPI0000172623; EMB
A;Note: only part of the coding region is given
C;Genetics:
A;Gene: pkpA
A;Introns: 60/1; 248/3; 277/2; 339/3; 534/1
C;Superfamily: Phycomyces blakesleeanus probable serine/threonine-spe
C;Keywords: phosphotransferase; protein kinase
F;34-289/Domain: protein kinase homology <KIN>
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Systim threonine-specific protein kinase pkpA (EC probable serine/threonine-specific protein kinase pkpA (EC c)Species: Phycomyces blakesleeanus (plate: 10-Sep-1999 #text_cherister: 10-Sep-1999 #text_cherister: 10-Sep-1999 #text_cherister: Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systim Systi
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A; Residues: 1-633 < RUI>
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                       CALEMAVLEIQTNGDT----
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                                                                      GDMGTAEMKNGKKYTV----
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23.7%;
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A;Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNA A;Residues: 1-1401 <CHU>A;Cross-references: UNIPROT:O14299; UNIPARC:UPI0000138F13; A;Cross-references: UNIPROT:O14299; UNIPARC:UPI0000138F13; C;Genetics: Store: strain 972h-; cosmid c9G1 C;Genetics: SPDB:SPAC9G1.02
A;Map position: 1
RESULT 11
$40482
$erine/threonine-specific protein kinase (EC serine/threonine-specific protein kinase (EC C;Species: Rattus norvegicus (Norway rat) C;Date: 19-May-1994 #sequence_revision 10-Nov C;Accession: $40482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP kinase kinase kinase - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_chang C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_chang C;Accession: T39225 C;Accession: T39225 R;Churcher, C.M.; Gentles, S.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1997
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A;Accession: T39225
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Pred. No. 8.1e-05;
O; Mismatches 135;
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                        10-Nov-1995
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RESULT 12
T51339
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DNA Res. 5, 341-348, 1998
A;Ritle: Molecular cloning and characterization of three cDNAs
A;Reference number: Z25272; MUID:99156228; PMID:10048483
                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitogen-activated protein kinase kinase (EC 2.7.1 N;Alternate names: MAP kinase kinase 4 C;Species Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UPI000017A3E7
C;Keywords: ATP; phosphotransferase; serine/threonine-specific F;267-520/Domain: protein kinase homology <KIN>F;275-283/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Manser, E.; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L. Nature 367, 40-46, 1994
A;Title: A brain serine/threonine protein kinase activated A;Reference number: S40482; MUID:94150588; PMID:8107774
                                                                                                                                          A;Description: (EC 2.7.1.-); mitogen-activated protein kinase kinase [va C;Superfamily: kinase-related transforming protein; protein kinase homol C;Keywords: phosphotransferase; protein kinase
                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-366 <ICH>
A; Cross-references: UNII
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A; Residues: 1-544 < MAN>
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A; Accession: S40482
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                                                                                                                                                                                                      C; Function:
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SSGSAPSSGGSASSTNTNSSIEAKNYSDLVRGNRIGSGAGGTVYKVIHRPSSRLYALKVI
                                    NQGNMPGLQSTFLAMDTEEGVE-----
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Pred. No. 4.4e-05;
                                                                                      Score 190; DB 2;
Pred. No. 3.1e-05;
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PII

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p21-activated protein kinase - human ("Species: Homo sagiens (man) (;Date: 21-Dec-1996 #sequence_revision 06-Jun-: C;Accession: G01773 R;Chernoff, J. submitted to the EMBL Data Library, April 1995 A;Reference number: G08374 A;Accession: G01773
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Best Local (
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                               RHSLSDPN-----MREFILCCLARDPARRPSAHSLIFHRVL 312
                                                                                                                                                                                                                                  SEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPII 172
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                                                                                                   PPEYGEVADGTAVDIFSFGMCALEM-----
                                                                                                                                HRDIKSDNILLGMDGSVKLTDFG---FCAQI----TPEQSKRSTMVGTPYWMA
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                                                                                                                                                                                                                                                                                                                                      PPDALTRNTEKOKKKPKMSDEE--ILEKLRSIVSVGDPKKKY-TRFEKIGOG---ASGTV
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                                                               PEVVTRKAYGPKVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNG----TPE----
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ilarity 24.6%;
Conservative 6
LQNPEKLSAIFRDFLNRCLDMDVEKRGSAKELLQHQFL
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                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 190; DE; Pred. No. 5.16 60; Mismatches
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5.1e-05;
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                                                                                              ----AVLEIQTNGDTRVTEEAIARA 276
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A;McCession: A57441
A;Molecule type: protein
A;Residues: 197-216;402,'S',404-409 <BEN>
A;Cross-references: UNIPARC:UDI000017A3BF; UNIPARC:UDI000017A3C0
A;Experimental source: placenta
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotran
F;247-501/Domain: protein kinase homology <KIN>
F;255-63/Region: protein kinase ATP-binding motif
F;197,402/Binding site: phosphate (Ser) (covalent) #status predic
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A;Residues: 1-30 <MAF>
A;Residues: 1-30 <MAF>
A;Cross references: UNIPARC:UPI000017A3BE
A;Cross references: UNIPARC:IPI000017A3BE
Chem: 70, Dennis, P.B.; Masaracchia, R.A.
J. Biol. Chem: 270, 21121-21128, 1995
A;Title: Activation of an 86/H4 kinase (PAK 65)
A;Reference number: A57441; MUID:95403344; PMID:
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EMBO J. 14, 1970-1978, 1995
A;Title: A novel serine kinase activated by rac1/CDC42Hs-dependent autophosphorylation A;Reference number: S55258; MUID:95262637; PMID:7744004
A;Accession: S55258
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NANLternate names: protein kinase PAK65; S6/H4 kinase
C;Species: Homo sapiens (man)
C;Date: 22-Aug-1996 #sequence revision 06-Sep-1996 #text_change 05-Oct-2004
C;Accession: S58682; S55258; S55304; S58690; A57441
R;Sells, M.; Knause, U.J.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernoff, J.
submitted to the EMBL Data Library, April 1995
A;Description: Human p21-activated protein kinases regulate actin organization in
A;Reference number: S58682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: S58690;
A;Contents: erratum
A;Accession: S58690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: UNIPARC: R; Martin, G.A.; Bollag, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 14, 4385, 1995
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A;Accession: S55304
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A; Residues: 'MEETQQKSNLEL', 31-89, 'T', 91-149, 'F', 151-224, 'T', 226-328, 'R', 330-338, 340-525
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A; Residues: 1-525 < SEL>
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GTPYWMAPEVVTRKAYGPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATNGTPELQ 465
                                                                                                                                                                                                                                                                                                                                                                                                                                      PVPAPVGDSHVDGAAKSLDKQKKKPKWTDEEIMEKLRTIVSIGDPKKKY-TRYEKIGQG-
                                                        NLHFF--PPEYGEVADGTAVDIFSFGMCALEM-----
                                                                                                                                                                                                                   ---FLDSYLVGDELFVVMEYLAGGSLTDVVTETACMDEAQIAAV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPAP-----RRAREREREREDESEDESDILEE-----SPCGRWQKRREQVNQGN
                                                                                                           A--NOVIHRDIKSDNVLLGMEGSVKLTDFG---FCAQI--
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23.6%; Pred. No. 6.6e-05;
ive 60; Mismatches 126;
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McCormick, F.;
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PMID:7673144
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                                                                                                        -TPEQSKRSTMV 405
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A,8tatus: preliminary
A,9tatus: preliminary
A,Molecule type: mRNA
A,Residuse: 1-544 <MAN>
A,FESIduse: 1-544 <MAN>
A,Cross-references: UNIPROT:Q62829; UNIPARC:UPI0000131225; GB:U33314; NID:g1039424; PIDN
C,Keywords: ATP
F,266-519/Domain: protein kinase homology <KIN>
F,274-282/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Manser, E.; Chong, C.; Zhao, Z.S.; Leung, T.; Michael, G.; Hall, C.; Lim, L. J. Blol. Chem. 270, 25070-25078, 1995
A;Title: Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK) A;Reference number: A57597; MUID:96027610; PMID:7559638
A;Accession: A57597
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//Alternate names: beta-PAK
C:Species: Rattus norvegicus (Norway rat)
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 31-Dec-2004
C:Accession: A57597
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Best Local S
Matches 87
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Local Similarity 24.6%; Pred. No. 7.4e-05;
nes 87; Conservative 57; Mismatches 119; Indels 91; Gaps
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                                                                                                                                                                                                                                                                                                374
                                                                                                                                                                                                                                                                                                                                                                                             323 PNIVN----YLDSYLVGDELWVVMEYLAGGSLTDVVTET-----CMDEGQIAAVCRECLQ 373
                                                                                                  478
                                                                                                                                      264 GDTRVTEBAIARARHSLSDPN-----MREFILCCLARDPARRPSAHSLLFHRVL 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 KIGQG---ASGTVYTALDIATGQEVAIKQMNL-----QQQPKKELIINEILVMRENKN 322
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                                                                                                                                                                                                                                                                                              ALDFLH--SNQVIHRDIKSDNILLGMDGSVKLTDFG---FCAQI-----TPEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                            PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILS 159
                                                                                            G----TPE-----LQNPERLSAVERDFLNRCLEMDVDRRGSAKELLQHPFL 519
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